GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

- protein search, using sw model OM protein Pebruary 23, 2006, 07:43:54 ; Search time 38 Seconds
(without alignments)
238.010 Million cell updates/sec Run on:

US-09-688-566-81 Perfect score: Title:

494 1 VSDVPRDLEVVAATFISRLI......VTDKSDTYKYDDPISINYRT Sequence:

94

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* PIR 80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	fibronectin precur	fibronectin - bovi			fibronectin - chic	fibronectin - Afri	probable tenascin	tenascin-X - bovin	restrictin precurs	tenascin precursor	janusin precursor,	tenascin-X precurs	leukocyte antigen-	tenascin precursor	cytotactin - chick		collagen alpha 1(V		tenascin-X - pig	protein-tyrosine-p	tenascin - eastern		collagen alpha 1(X		protein-tyrosine-p	protein-tyrosine-p	fibronectin, trans		protein-tyrosine-p
SUM	O.	FNHU	FNBO	S14428	A28512	A29355	A43908	T09070	T42629	JH0675	S19694	A45445	A40701	546216	JQ1322	A31930	A32230	A54849	A32160	S65944	A56178	A43902	A56493	A40020	A40970	D54689	C54689	S00848	150213	
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	Length	2386	2265	2477	273	1020	2481	4006	4135	1353	1746	1356	3566	1898	2019	933	1810	2944	2201	417	1912	647	1290	3124	843	1691	1894	147	440	
d	Query Match	73.1	71.7	67.4	63.0	63.0	53.0	25.3	25.1	24.5	24.5	23.5	22.5	22.4	22.3	21.9	21.9	21.6	21.3	20.6	20.5	19.9	19.4	19.4	19.0	18.6	18.6	18.5	18.3	
	Score	361	354	333	311	311	262	125	124	N	121	116	111	110.5	110	108	108	106.5	105	102	100	98.5	96	96	94	92	92	91.5		
	Result No.	-	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

tenascin - rat (fr fibronectin ED-B -	leukocyte antigen- protein-tyrosine-p tenascin-X - mouse	fibronectin ED-A - nephrin - human	cype XII collagen	collagen alpha 1(X collagen alpha 1(X tenascin Y precurs	protein-tyrosine-p protein-tyrosine-p	undulin 2 - human hypothetical prote
A54861 I46162	TDHULK A55148 I48839	146161 T37190	151027 A45974	S31212 S78476 T42635	TDFFLK 138670	B40970 A90255
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88.5	86 83 83	85	81.5 81.5	81.5 81.5 80	79 78	77.5
30	3 3 3 4 3 5	36.3	38	4 4 4 0 0 1	43	4 4 5

ALIGNMENTS

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fibronectin precursor [validated] - human
N.Alternate names: fibronectin splice form ED-A
C;Species: Homo Sapiens (man)
C;Species: Homo Sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2004
C;Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22
R;Dean, D.C.; Bowlus, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A;Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A;Reference number: A26460; MUID:87175578; PMID:3031656

A; Molecule type: DNA
A; Residues: 1.49 - OEBAA; Residues: 1.49 - OEBAA; Cross-references: UNIPROT: P02751; UNIPROT: Q14327; UNIPARC: UPI000016A926; GB: M15801; NI
R; Oldberg, A.; Ruoslahti, B.
B; Oldberg, A.; Ruoslahti, B.
A; Title: Chem. 261, 2113-2116, 1986
A; Title: Evolution of the fibronectin gene.
A; Reference number: A26284; MUID: 86111901; PMID: 3003095

A;Accession: A26284

A; Molecule type: DNA A; Residues: 1447-1540 <old>
A; Residues: 1447-1540 <old>
A; Cross-references: UNIPARC: UPI0000112E37; GB:M12549; NID:g182688
A; Cross-references: UNIPARC: UPI0000112E37; GB:M12549; NID:g182688
A; Note: the authors translated the codon TTC for residue 1494 as Glu
R; Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
R; Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
A; Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B
A; Reference number: S00848; MUID:88233940; PMID:3375063

A, Accession: S03917

A,Molecule type: DNA A,Residues: 1554-1767, 'V',1769-1783 <PAO> A,Cross-references: UNIPARC:UPI000017432B; EMBL:X07718; NID:g31402 A,Note: the authors translated the codon AAC for residue 1631 as Asp R;Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E. ERSB Lett. 207, 287-291, 1986 A;Title: Donor and acceptor splice signals within an exon of the human fibronectin gene: A;Reference number: A24854; MUID:87030929; PMID:3770201

A:Accession: A24854

A,Molecule type: DNA A,Residues: 1992-2147 «VIB> A,Kresidues: 1992-2147 «VIB> A,Cross-references: UNIPARC:UP1000017432C; GB:X04530; NID:g31436 R;Gutman, A.; Yamada, K.M.; Kornblihtt, A. BSBS Lett. 207, 145-148, 1986 A;Title: Human fibronectin is synthesized as a pre-propolypeptide. A,Reference number: A24476; MUID:87030890; PMID:3770189

A;Accession: A24476 A;Status: not compared with conceptual translation

A;Molecule type: mRNA
A;Residues: 1-14,'Q',16-38 <GUT>
A;Residues: 1-14,'Q', 16-38 <GUT>
A;Cross-references: UNIPARC:UPI000017432D
B;Kornblintt, A.R.: Unezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985

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Cross-references: GDB:119135; OMIM:135600
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;Residues: 1589-1630,'T',1722-2058 <GAR3>;Cross-references: UNIPARC:UP1000017433A
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A,Molecule type: protein
A,Residues: 233-301 <GRI>A;Cross-references: UNIPARC:UPI0000174338
R;Calaycay, J.; Pande, H.; Lee, T.; Borsi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 616-677,'Q',679-703,'PT' <CAL:
A;Cross-references: UNIPARC:UP10000174339
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A; Residues: 2071-2080;2112-2356 <GAR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: A23901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A23891
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                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 32-1344,1346-2080;2112-2386 <KOR>
A;Cross-references: UNIPARC:UP1000017432F; UNIPARC:UP1000017432F; GB:X02761
A;Cross-references: UNIPARC:UP1000017432F; UNIPARC:UP1000017432F; GB:X02761
B;Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.B.
Nucleic Acids Res. 12, 5853-5868, 1984
A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A;Reference number: A93529; MUID:84272258; PMID:6462919
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A; Residues: 1978-1990, 2016-2018, N', 2020-2081, 2113-2127 <SEK>
A; Residues: 1978-1990, 2016-2018, N', 2020-2081, 2113-2127 <SEK>
A; Cross-references: UNIPARC: UPI000006E04C; GB:M14060; NID:g182701; PIDN:AAA52464.1; PID:
R; Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Froc. Natl. Acad. Sci. US.A. 80, 321843-3222, 1983
A; Title: Isolation and characterization of CDNA clones for human and bovine fibronectine
A; Reference number: A21165; MUID:83221567; PMID:6304699
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosseluces: 2291-2386 (xO3-
A;Cross-references: UNIPARC:UPI0000174334; GB:K00799; NID:g182681; PIDN:AAA52460.1; PID:
B;Garcia-Pardo, A.; Pearlstein, B.; Frangione, B.
A; Biol. Chem. 258, 12670-12674, 1983
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A92398; MUID:84032463; PMID:6630202
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A,Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>
A,Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>
R,Crose-references: UNIPARC: UD10000174335
R,Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A,Title: Further characterization of the binding of fibronectin to gelatin reveals the physecesion: S34791; MUID: 93312001; PMID: 8323285
                       at
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A, Residues: 1594-2386 cBER>
A, Residues: 1594-2386 cBER>
A, Residues: 1594-2386 cBER>
B, Unwezawa, K.; Kornblihtt, A.R.; Baralle, R.E.
FEBS Lett. 186, 31-34, 1985
A, Title: Isolation and characterization of CDNA clones for human liver fibronectin. A, Reference number: A2245; MUID: 85231203; PMID: 2989004
A, Reference number: A2245; MUID: 85231203; PMID: 2989004
A, Residues: 1948-2067 cUME>
A, Residues: 1978-1991; 2017-2039 cUMZ>
A, Residues: 1975-1991; 2017-2039 cUMZ>
A;Title: Primary structure of human fibronectin: differential splicing may generate A;Reference number: A91008; MUID:85284965; PMID:2992939
A;Accession: A91008
A;Status: nucleic acid sequence not shown
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Calaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.B.; Zardi, L. Balol. Chem. 260, 12136-12141, 1985.
; Title: Primary structure of a DNA-and heparin-binding domain (domain III) in human ple; Reference number: A23901; MUID:86008277; PMID:3900070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UP10000174339
R;Pierschbacher, M.D.; Ruoslahti, B.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A;Title: The cell attachment domain of fibronectin. Determination of the primary structum A;Reference number: A92386; MUID:82265604; PMID:7050098
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Title: Human plasma fibronectin. Demonstration of structural differences between the A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
Bitol. Chem. 260, 10320-10325, 1985
;Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dalti
;Reference number: A23891; MUID:85261459; PMID:4019516
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A;Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
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C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicatin
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-31/Domain: propeptide #status predicted <PRO>
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C;Comment: The extra domain and connecting strand 3 are subject to developmental and tis
C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins, attion, and transformation.
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A;Rocession: A92386
A;Rosidues: 1441-1548 <PIE>
A;Cross-references: UNIPARC:UPI0000141CD5
A;Cross-references: UNIPARC:UPI0000141CD5
A;Note: residues: 1524-1527 are responsible for the cell-binding activity
B;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa A;Reference number: A32517; MUID:87241275; PMID:3593230
A;Accession: A32517
A;Residues: 291-300;551-560 cGAR2>
A;Cross-references: UNIPARC:UP10000174336; UNIPARC:UP10000174337
R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
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F;52-37/Domain: fibronectin type I repeat homology <1F1>
F;97-135/Domain: fibronectin type I repeat homology <1F2>
F;141-179/Domain: fibronectin type I repeat homology <1F3>
F;186-225/Domain: fibronectin type I repeat homology <1F3>
F;31-270/Domain: fibronectin type I repeat homology <1F5>
F;31-270/Domain: collagen binding <CBR>
F;308-342/Domain: fibronectin type I repeat homology <1F5>
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Residues: 1614-1630,'T',1722-2081,2113-2244 <TRE>
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A; Cross-references: UNIPARC: UPI0000177AEB
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Matches
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A; Readdues 1.16, °C', 18-20, °S', 22-412;447-463;1367-1517;1567-1673;2062-2176, N', 2178-226
A; Cross-references: UNIPARC: UPI000017433E; UNIPARC: UPI0000174340;
C; Comment: The plasma fibronectin molecule consists of two chains, which are connected by C; Comment: The plasma fibronectin molecule consists of two chains, which are connected by C; Comment: Plasma fibronectin is synthesized by hepatocytes.
C; Comment: Plasma fibronectin is synthesized by hepatocytes.
C; Comment: Plasma fibronectin is synthesized by hepatocytes.
C; Superfamily: fibronectin fibronectin type I repeat homology; fibronectin type I repeat homology of P; 21-241/Domain: fibronectin type I repeat homology of P; 21-246/Domain: fibronectin type I repeat homology of P; 21-246/Domain: fibronectin type I repeat homology of P; 21-241/Domain: fibronectin type III repeat homology of P; 21-241/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Mesidues: 1-2265 csRO.
A;Residues: 1-2265 csRO.
A;Cross-references: UNIPROT:P07589; UNIPARC:UP1000012A7BB
R;Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
R;Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
A;C.; Maltl. Acad. Sci. U.S.A. 96, 23128-3322, 1988
A;Title: Isolation and characterization of CDNA clones for human and bovine fibronectins A;Reference number: A21165; MUID:83221567; PMID:6304699
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A; Residues: 2170-2265 «KOR»
A; Residues: 2170-2265 «KOR»
A; Residues: 2170-2265 «KOR»
A; Residues: 2170-2265 «KOR»
A; Cross-references: UNIPARC: UPI000016C30C; GB: K00800; NID: 916375; PIDN: AAA30521.2; PID: R; Petersen, T.E.; Thogersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr Proc. Natl. Acad. Sci. U.S. A. 80, 137-141, 1983
A; Title: Partial primary structure of bovine plasma fibronectin: three types of internal A; Reference number: A23292; MUID: 83117805; PMID: 6218503
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26452; B21165; Ā23228]
C;Accession: A26452; B21165; Ā2328]
C;Accession: A26451; Barsen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S. Bur, J. Biochem. 161, 441-453, 1986
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                                                                                                                                                                                                                                                                            Score 361; DB 1; Length 23
Pred. No. 1.8e-28;
4; Mismatches 17; Indels
F;360-401/Domain: fibronectin type II repeat homology <2F1:
F;420-461/Domain: fibronectin type II repeat homology <2F2:
F;470-508/Domain: fibronectin type I repeat homology <1F7:
F;518-555/Domain: fibronectin type I repeat homology <1F9:
F;561-599/Domain: fibronectin type I repeat homology <1F9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                 73.18;
                                                                                                                                                                                                                                                                   Query Match 73.1
Best Local Similarity 77.7
Matches 73; Conservative
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Fil/Modified site: pyrrolidone carboxylic acid (Gln) status experimental
Fi3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experime
Fi21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-3
Fi215-47,74-2200,2198-2209/Disulfide bonds: #status predicted
Fi399,497,511,846,966,1213,1987/Binding site: carbohydrate (Asn) (covalent) #status expe
Fi105,1692/Binding site: carbohydrate (Asn) (covalent) #status absent
Fi1944/Binding site: carbohydrate (Thr) (covalent) #status experimental
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A;Residues: 1-2477 <HTN>
A;Residues: 1-2477 <HTN>
A;Cross-references: UNIPROT:P04937; UNIPPAC:UPI000012A7C6; EMBL:X15906; NID:g56163; PIDN
R;Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A;Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A;Reference number: S12455; MUID:88054951; PMID:2445560
A;Status: nucleic acid sequence not shown
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A;Crosdes: 609-1810, Tr,1812-2283 <SCH>
A;Crosderedes: 609-1810, Tr, 1812-2283 <SCH>
A;Crosderedes: UNIPARC:UPI0000177AEA; EMEL:X15906

R;Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.

Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984

A;Title: A single rat fibronectin gene generates three different mRNAs by alternative sp
A;Reference number: A22319; MUID:84298097; PMID:6089177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
R;Hynes, R.O.
Bubmitted to the EMBL Data Library, July 1989
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F;105-1134/Domain: fibronectin type III repeat homology <FN3F>
F;1142-1227/Domain: fibronectin type III repeat homology <FN3G>
F;135-1134/Domain: fibronectin type III repeat homology <FN3G>
F;135-1404/Domain: fibronectin type III repeat homology <FN3I>
F;1410-1517/Domain: cell attachment <CAD>
F;1410-1502/Domain: fibronectin type III repeat homology <GN3I>
F;1416-1502/Domain: fibronectin type III repeat homology <FN3J>
F;1600-1807/Domain: heparin binding <HBC-
F;1600-1807/Domain: fibronectin type III repeat homology <FN3L>
F;1600-1773/Domain: fibronectin type III repeat homology <FN3L>
F;1601-1773/Domain: fibronectin type III repeat homology <FN3N>
F;1781-1863/Domain: fibronectin type III repeat homology <FN3N>
F;1801-1972/Region: cell attachment (R-G-D) motif
F;1982-2062/Domain: fibronectin type III repeat homology <FN3N>
F;1982-2062/Domain: fibronectin type III repeat homology <F
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F;2385-2420/Domain: fibronectin type I repeat homology
                                                                                                                                                                                                                                                        67.4%;
68.1%;
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                                                                                                                                                                                                                                                                                                                                 64; Conservative
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Best Local Similarity
Matches 64; Conserv
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                                                                                                                                                 A,Accession: S46203
A,Accession: S46203
A,Molecule type: protein
A,Residues: 1183-1192; GLN',1268,'P',1270-1271,'D',1273,'CF',1276,'PY';1385-1399 <FAL>
A,Cross-references: UNIPARC:UP10000177AEC; UNIPARC:UP10000177AED; UNIPARC:UP10000177AEB
R,Patell, R.S.; Odermatt, B.; Schwarzbauer, J.B.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1997
A,Title: Organization of the fibronectin gene provides evidence for exon shuffling durin
A,Reference number: S00459; MUID:88054950; PMID:3119323
A,Residues: 1-139;2382-247, APAT>
A,Residues: 1-139;2382-247, APAT>
A,Residues: 1-139;2382-247, APAT>
A,Cross-references: UNIPARC:UP1000017095C; UNIPARC:UP10000177AEF; EMBL:X05831
A,Note: the authors translated the codon CCT for residues 51 and 94 as Ala
R,Schwarzbauer, J.B.; Tamkun, J.W.; Lemlschka, I.R.; Hynes, R.O.
Cell 35, 421-431, 1983
A,Title: Three different fibronectin mRNAs arise by alternative splicing within the codi
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Aintrons: 51/1; 94/1; 2416/3; 2454/3
Aintrons: 51/1; 94/1; 2416/3; 2454/3
Aintrons: 51/1; 94/1; 2416/3; 2454/3
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CiSupordas: alternative splicing cell adhesion; collagen binding; disulfide bond; dupli F;1-32/Domain: signal sequence #status predicted <51G>
F;3-84/JOMAIN: fibronectin #status predicted <51G>
F;3-84/Domain: fibronectin type I repeat homology <1F>
F;3-84/Domain: fibronectin type I repeat homology <1F>
F;38-136/Domain: fibronectin type I repeat homology <1F>
F;38-142/Domain: fibronectin type I repeat homology <1F>
F;38-142/Domain: fibronectin type I repeat homology <1F>
F;38-142/Domain: fibronectin type II repeat homology <1F>
F;38-142/Domain: fibronectin type III repeat homology <1F>
F;38-142/Domain: fibronectin type III repeat homology <1F>
F;38-143/Domain: fibronectin type III repeat homology <1F>
F;38-144/Domain: fibronectin type III repeat homology <1F>
F;144-152/Domain: fibronectin type III repeat homology <1F>
F;141-152/Domain: fibronectin type III repeat homology <1F>
F;141-153/Domain: fibronectin type III repeat homology <1F>
F;141-154/Domain: fibronectin type III repeat homology <1F>
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F;141-158/Domain: fibronectin type III repeat homology <1F>
F;141-158/Domain: fibronectin type III repeat homology <1F>
F;141-158/Domain: fibronectin type III repeat homolog
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R;Falkenberg, C.; Enghild, J.J.; Thogersen, I.B.; Salvesen, G.; Akerstroem, B. Biochem. J. 301, 745-751, 1994
A;Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in A;Reference number: S46203; MUID:94330948; PMID:7519849
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A;Residues: 1722-1810 <RES>
A;Cross-references: UNIPARC:UPI00000040C; GB:M11750; NID:G204164; PIDN:AAA41170.1; PID:
C;Genetics:
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R;Odermatt, E.; Tamkun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A;Title: Repeating modular structure of the fibronectin gene: Relationship to protein
A;Reference number: 159049; MUID:86016741; PMID:3863113
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fibronectin type I repeat homology <1F10>
fibronectin type I repeat homology <1F11>
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A,Molecule type: mRNA
A,Residues: 1586-1720,'T',1722,1813-2477 <SC2>
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Cincession: A28512
Riwbomura, S.; Obara, M.; Karasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, K. Riwbomura, S.; Obara, M.; Karasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, K. Biochim. Biophys. Acta 910, 171-181, 1987
A;Title: Genetic analysis of the cell binding domain region of the chicken fibronectin gel A;Title: Genetic analysis of the cell binding domain region of the chicken fibronectin gel A;Reference number: A28512; MUID:88050950; PMID:2823899
A;Accession. A28512
A;Molecule type: DNA
A;Residues: 1-273 <KUB>
A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: 80/1; 129/1; 184/1; 236/1
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics: A;Mote: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
A;Mote: the authors translated
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R;Norton, P.A.; Hynes, R.O.
Mol. Cell. Biol. 7, 497-4307, 1987
Mol. Cell. Biol. 7, 497-4307, 1987
A;Title: Alternative splicing of chicken fibronectin in embryos and in normal and transfic A;Title: Alternative A29355; MUID:88142820; PMID:2830487
A;Reference number: A29355; MUID:88142820; PMID:2830487
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F;53-79,77-88,98-126,124-136,142-170,168-180,187-216,214-226,232-261,259-271,308-335,333
88,2366-2378,2385-2411,2409-2420/Dishlide bonds: #status predicted
F;2458/Disulfide bonds: interchain (to 2462) #status predicted
F;2462/Disulfide bonds: interchain (to 2458) #status predicted
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A28512
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C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
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A; Residues: 1-1020 <NOR>
A; Cross-references: UNIPROT: P11722; UNIPARC: UPI0000177AES
C; Genetics:
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Pred. No. 1.4e-25;
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A; Accession: T09070
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A. Molecule type: mRMA
A. Residues 1-2481 - DBS.
A. Cross-references: UNIPARC.UPTORO0171AR7; GB:W77920
A. Residues 1-2481 - DBS.
A. Cross-references: UNIPARC.UPTORO0171AR7; GB:W77920
C. Superfamily: fibromectin; Edward in type I repeat homology; fibromectin type I repeat homology accessed and accessed in the content of the conten
                      duplication; extracellular matrix; glycoprotein; heter
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
R;Desimone, D.W.; Norton, P.A.; Hynes, R.O.
Dev. Biol. 149, 357-369, 1992
A;Title: Identification and characterization of alternatively spliced fibronectin mRNAs
A;Reference number: A43908
A;Accession: A43908
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C; Keywords: alternative splicing; duplication; extracellular matrii P;1-86/Domain: fibronectin type III repeat homology <FN31> P;92-177/Domain: fibronectin type III repeat homology <FN31> F;180-262/Domain: fibronectin type III repeat homology <FN33> P;257-259/Region: cell attachment (R-G-D) motif P;24-356/Domain: fibronectin type III repeat homology <FN3K> F;364-446/Domain: fibronectin type III repeat homology <FN3K> F;546-628/Domain: fibronectin type III repeat homology <FN3N> F;546-628/Domain: fibronectin type III repeat homology <FN3N> F;636-718/Domain: fibronectin type III repeat homology <FN3N> F;636-718/Domain: fibronectin type III repeat homology <FN3N> F;646-628/Domain: fibronectin type III repeat homology <FN3N> F;640-379/Domain: fibronectin type III repeat homology <FN3O> F;640-979/Domain: fibronectin type III repeat homology <FN3O> F;940-979/Domain: fibronectin type III repeat homology <FN3O> F;940-979/Domain: fibronectin type II repeat homology <FN3O> F;940-979/Domain: fibronectin type II repeat homology <FN3O> F;940-979/Domain: fibronectin type II repeat homology <FN3O> F;940-969,967-979/Domain: fibronectin type III repeat homology <FN3O> F;940-979/Domain: fibronectin type III repeat homology <FN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 311; DB 2; Length 1020; 64.9%; Pred. No. 9e-24; ive 11; Mismatches 22; Indels
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61; Conservative 1
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Matches 61; Conserv
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F;2197-2277/Domain: fibronectin type III repeat homology <FN3Q>
F;2304-2340/Domain: fibronectin type I repeat homology <FR10>
F;2346-2383/Domain: fibronectin type I repeat homology <1F10>
F;2340-2453/Domain: fibronectin type I repeat homology <1F11>
F;2390-2453/Domain: fibronectin type I repeat homology <1F12>
F;55-81,79-90,100-128,126-138,144-172,170-182,189-218,216-228,234-263,261-273,309-336,33
F;2453/Disulfide bonds: interchain (to 2463) #status predicted
F;2453/Disulfide bonds: interchain (to 2463) #status predicted
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A; De
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A;Residues: 1-4006 <ROW>
A;Cross-references: UNIPROT:035452; UNIPARC:UPI000002A159; EMBL:AF030001; NID:92564945;
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R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1538 VSDVPTDLEVTSSSPNTLTISWEAPAVSVRYYRITYSQTGGHGPEKEFTVPGTSNTATIR 1597
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N;Alternate names: flexilin
C;Species: Bos primigenius taurus (cattle)
C;Date: il-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.0%; Score 262; DB 2; Length 2481; 53.2%; Pred. No. 2.6e-18; tive 16; Mismatches 28; Indels (
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R;Elefteriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, J. Biol. Chem. 272, 22866-22874, 1997
A;Title: Characterization of the bovine tenascin-X.
A;Reference number: Z22180; MUID:97426436; PMID:9278449
A;Accession: T42629
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nes 50; Conservative
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us-09-688-566-81.rpr

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A, Molecule type: mRNA
A, Residues: 1-1746 <NIS>
A, Residues: 1-1746 <NIS>
A, Residues: 1-1746 <NIS>
A, Cross-references: UNIPROT: Q29116; UNIPARC: UPI0000136BBB; EMBL: X61599; NID: 92124; PIDN: C; Superfamily: tenascin; EGF homology; fibrinding beta/gamma homology; fibronectin type IC; Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracellt F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 23-1746/Product: tenascin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydrate (Asn) (covalent) #sta
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Nighternate names: neural recognition glycoprotein J1-160/180, short form
Cippecies: Rattus norvegitus (Norway rat)
Cipate: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
Airclession: A45445
Airclession: A45445
Airclession: A45445
Airclession: Preliminary
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A;Residues: 1-1356 <FUS>
A;Cross-references: UNIPROT:Q05546; UNIPARC:UP100000E6D8A; GB:Z18630; NID:957961; PIDN:C?
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                                                                                                                                                                                                                                                                                     tenascin precursor - pig
N'Alternate names: contactin; hexabrachion
C.Species: Sus scrofa domestica (domestic pig)
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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F;346-372/Domain: EGF homology <EGF>
F;37-403/Domain: EGF homology <EGF>
F;37-403/Domain: Edronectin type III repeat homology <FN3A>
F;711-793/Domain: Eibronectin type III repeat homology <FN3B>
F;802-884/Domain: Eibronectin type III repeat homology <FN3C>
F;892-976/Domain: Eibronectin type III repeat homology <FN3C>
F;984-1064/Domain: Eibronectin type III repeat homology <FN3E>
F;1073-1155/Domain: Eibronectin type III repeat homology <FN3F>
F;164-1246/Domain: Eibronectin type III repeat homology <FN3G>
F;124-1335/Domain: Eibronectin type III repeat homology <FN3G>
F;1343-1423/Domain: Eibronectin type III repeat homology <FN3G>
F;1341-1511/Domain: Eibronectin type III repeat homology <FN3G>
F;1841-1511/Domain: Eibronectin type III repeat homology <FN3G>
F;1826-1334/Domain: Eibrinogen beta/gamma homology <FN3G>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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A;Residues: 1-772,863-1356 <FU2>
                      744 EPGTEYTISIIA 755
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1353 <nOE>
A;Cross-references: UNIPROT:Q00546; UNIPARC:UPI00000FC0A7; GB:X64649; NID:g63613; PIDN:CA;Experimental source: brain
A;Residues: 579-586;827-840 <nOEI>
A;Molecule type: protein
A;Residues: 579-586;827-840 <nOEI>
A;Cross-references: UNIPARC:UPI0000174344; UNIPARC:UPI0000174345
C;Comment: This protein is a neural extracellular matrix protein implicated in neural of S;Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin type; C;Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin type; E;1-33/Domain: signal sequence #status predicted <sIG>
F;1-33/Domain: signal sequence #status predicted <AIC>
F;34-1353/Product: restrictin #status predicted <AMT>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: Translated from GB/EMBL/DDBJ
A;Kossiues: 1-4135 < ELES
A;Cross-references: UNIPROT:018977; UNIPARC:UP100001101C4; EMBL:Y11915; NID:G2462978; PI
C;Genetics:
A;Gene: TN:
C;Superfamly: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
C;Keywords: extracellular matrix; glycoprotein; heptad repeat
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F;1130-1338/Domain: fibrinogen beta/gamma homology <FBG>
F;122-1286/Region: calcium binding #status predicted
F;53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequenc. 22 zevision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0675; PS0386; S2254
R;Noerenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
Neuron 8, 849-863, 1992
A;Teile: The chicken neural extracellular matrix molecule restrictin: similarity with
A;Reference number: JH0675; MUID:92265298; PMID:1375037
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; Pred. No. 0.00037;
13; Mismatches 28; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 4135;
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F313-494/Domain: fibronectin type III repeat homology <FN2>
F502-584/Domain: fibronectin type III repeat homology <FN3>
F592-676/Domain: fibronectin type III repeat homology <FN3>
F384-764/Domain: fibronectin type III repeat homology <FN4>
F384-764/Domain: fibronectin type III repeat homology <FN5>
F372-853/Domain: fibronectin type III repeat homology <FN5>
F861-941/Domain: fibronectin type III repeat homology <FN5>
F861-941/Domain: fibronectin type III repeat homology <FN5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.1%; Score 124; DB 2; Best Local Similarity 35.9%; Pred. No. 0.00065; Matches 33; Conservative 17; Mismatches 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 KPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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Matches 29; Conservative
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A; Map position: 6p21.3-6p21.3
C; Superfamily: BGF homology; fibringen beta/gamma homology; fibronectin type III repeat C; Superfamily: BGF homology; fibringen beta/gamma homology; fibronectin type III repeat homology astrones.
F; 435-461/Domain: Eibronectin type III repeat homology astrones.
F; 873-955/Domain: fibronectin type III repeat homology astrones.
F; 873-955/Domain: fibronectin type III repeat homology astrones.
F; 873-955/Domain: fibronectin type III repeat homology astrones.
F; 1078-1158/Domain: fibronectin type III repeat homology astrones.
F; 1078-1158/Domain: fibronectin type III repeat homology astrones.
F; 1078-1159/Domain: fibronectin type III repeat homology astrones.
F; 1167-1247/Domain: fibronectin type III repeat homology astrones.
F; 1167-1247/Domain: fibronectin type III repeat homology astrones.
F; 1168-1159/Domain: fibronectin type III repeat homology astrones.
F; 1168-1169/Domain: fibronectin type III repeat homology astrones.
F; 1168-1169/Domain: fibronectin type III repeat homology astrones.
F; 1168-1169/Domain: fibronectin type III repeat homology astrones.
F; 1168-1141/Domain: fibronectin type III repeat homology astrones.
F; 1167-224/Domain: fibronectin type III repeat homology astrones.
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NyAlternate names: leukocyte common antigen homolog
NyAlternate names: leukocyte common antigen homolog
NyAlternate names: leukocyte common antigen homolog
NyContains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
N;Zhang, W.R.; Hashimoto, M.; Ahmad, F.; Ding, W.; Goldstein, B.J.
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho
A;Reference number: 546216; MUID:94347119; PMID:8068021
A;Accession: 546216
A;Accession: 546216
A;Accession: 646216
A;Accessi
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fibronectin type III repeat homology <3827>
fibronectin type III repeat homology <3828>
fibrinogen beta/gamma homology <866>
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                                                              A, Note: sequence extracted from NCBI backbone (NCBIP:95694)
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                                                                                                                                                                A;Gene: GDB:TNXA; D6S103B; TNX; XA; XB
A;Crose-references: GDB:568487; OMIM:600261
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Matches 30; Conserv
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A; Description: Molecular characterization and in situ mRNA localization of the neural red; A; Reference number: S32023
A; A; Reference number: S32023
A; Accession: S32023
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1356 < FUS2>
A; Cross-references: UNIPARC: UPI00000E6DBA; EMBL: Z18630; NID:957961; PIDN: CAA79229.1; PID
C; Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
C; Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
C; Superfamily: nestrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin; typ
C; Meywords: alternative splicing; duplication; extracellular matrix; glycoprotein; olige
F; 1-772, 863-1356/Product: janusin, short form #status experimental <ALT>
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A;Status: preliminary
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-3566 - BRI>
A;Cross-references: UNIPROT:P22105; UNIPROT:Q9UC11; UNIPARC:UP10000174343; EMBL:X71937
A;Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/CARAFETENCE number: A33725; MUID:89367293; PMID:2475872
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A;Residues: 2748-3199, VV, 3201-3298, E', 3299-3314, G', 3316-3566 <MOR>
A;Residues: 2748-3199, VV, 3201-3298, E', 3299-3314, G', 3316-3566 <MOR>
A;Crose-references: UNIPARC:UP1000016A98B; GB:M25813; NID:g183069; PIDN:AAA35884.1; PID:
B;Matsumcto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.
Genomics 12, 485-491, 1992
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744 EPGAEYIISITAERGRQQSLESTVDAFTGFRPISHLHFSHVİSSSVNITWSDFSPADRL 803
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: A40701; A3725; C42175
R;Bristow, J; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.
J. Cell Biol. 1122, 265-278, 1993
A;Title: Tenascin-X: a novel extracellular matrix protein encoded by the hum
A;Reference number: A40701; MUID:99300909; PMID:7686164
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F;1133-1341/Domain: fibrinogen beta/gamma homology <FBG>
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F;235-261/Domain: EGF homology <EG2.
F;235-261/Domain: EGF homology <EG3.>
F;297-323/Domain: EGF homology <EG4.>
F;297-323/Domain: EGF homology <EG4.>
F;297-324/Domain: fibronectin type III repeat homology <FN1.>
F;413-494/Domain: fibronectin type III repeat homology <FN2.>
F;502-694/Domain: fibronectin type III repeat homology <FN3.>
F;684-64/Domain: fibronectin type III repeat homology <FN4.>
F;684-64/Domain: fibronectin type III repeat homology <FN4.>
F;684-64/Domain: fibronectin type III repeat homology <FN4.>
F;684-64/Domain: fibronectin type III repeat homology <FN4.
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Fred. No. 0.0012;
18; Mismatches 3
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A;Residues: 1849-1936 <MAT>
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Best Local Similarity
Matches 34; Conserv
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A;Residues: 1-2019 <SAG>
A;Cross-references: UNIPROT:Q64706; UNIPARC:UPI000005D89C; GB:D90343; NID:g220609; PIDN:E
A;Experimental source: cell line 2H6GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Note: the authors translated the codon ATG for residue 60 as Trp
R;Weller, A.; Beck, S.; Ekblom, P.
J. Cell Biol. 112, 355-362, 1991
A;Title: Amino acid sequence of mouse tenascin and differential expression of two tenasco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA

A; Rosidues: 1-201, E', 203-317, S', 319-620, 622-1010, N', 1012-1018, S', 1020-1024, H', 1026-3

A; Ross-references: UNIPARC:UP10000174346; GB:X56304

A; Accession: B37936

A; Status: preliminary; nucleic acid sequence not shown

A; Molecule type: mRNA

A; Residues: 1-201, E', 203-317, S', 319-620, 622-1010, N', 1012-1018, S', 1020-1024, H', 1026-3

A; Ross-references: UNIPARC:UP1000174347; GB:X56304

R; Weller, A.; Beck, S.; Ekblom, P.

submitted to the EMBL Data Library, August 1990
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A; Title: Analysis of aggreen and tenascin gene expression in mouse skeletal tissues by 19, 4, 11; 16: Analysis of aggreen and tenascin gene expression in mouse skeletal tissues by 19, 13; Reference number: S50206; MUID:9503091; PMID:7524681
A; Reference number: S50209
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: MRNA
A; Readudes: 46-146 cd.10.
A; Cross-references: UNIPARC:UPI0000174348; EMBL:X80281
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C; Superfamily: EGF homology; fibrinogen beta/gamma homology; fibronectin type III repeat Corm #status predicted cMAT>
F; 22-2019/Product: tenascin, long splice form #status predicted cMAT>
F; 22-2019/Product: tenascin, short splice form #status predicted cMAT>
F; 22-2019/Product: tenascin, short splice form #status predicted cMAT>
F; 22-2019/Product: thype III repeat homology cFN3A>
F; 22-2019/Domain: fibronectin type III repeat homology cFN3B>
F; 802-894-1064/Domain: fibronectin type III repeat homology cFN3F>
F; 103-1155/Domain: fibronectin type III repeat homology cFN3F>
F; 103-1155/Domain: fibronectin type III repeat homology cFN3F>
F; 104-11458/Domain: fibronectin type III repeat homology cFN3F>
F; 104-1169/Domain: fibronectin type III repeat homology c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: Aminoacid sequence of mouse tenascin and differential expression of two A;Reference number: S14571
A;Accession: S14571
     A;Title: Murine tenascin: cDNA cloning, structure and temporal expression of isoforms.
A;Reference number: JQ1322; MUID:92009211; PMID:1717349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-201, 'E', 203-317, 'S',319-1018, 'S',1020-1024,'H',1026-1305, 'S',1307-2019
A;Cross-references: UNIPARC:UP1000002A093; EMBL:X56304; NID:954768; PIDN:CAA39751.1;
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Pred. No. 0.0079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A37936; MUID:91107734; PMID:1703162
A;Accession: A37936
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                                                                                                                         A;Accession: JQ1322
A;Status: nucleic acid sequence not shown
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Best Local Similarity
Matches 34; Conserv
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A;Cross-references: UNIPARC:UPI0000177056; UNIPARC:UPI0000177057
A;Cross-references: UNIPARC:UPI0000177056; UNIPARC:UPI0000177057
A;Pot. D. A.; Woodford, T.A.; Remboutsika, B.; Haun, R.S.; Dixon, J.E.
J. Biol. Chem. 266, 19688-19696, 1991
A;Title: Cloning, bacterial expression, purification, and characterization of the cytopl
A;Reference number: A41032; MUID:92011772; PMID:1918076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CJR Expwords: duplication; glycoprotein; phosphoric monoester hydrolase; the principle of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A33154
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1035-1072, 'S', 1074-1433, 'T',1435-1638,'N',1640-1642,'HT',1645-1898 <PO2>
A;Cross-references: UNIPARC:UPIO0001709F3
C;Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatas
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Accession: A41032
A.Molecule type: mRNA
A;Residues: 1035-1072, 8',1074-1433,'T',1435-1638,'N',1640-1642,'HT',1645-1898 <POT>
A;Cross-references: UNIPARC:UPI00001709F9; GB:M60103; NID:g205130; PIDN:AAA41510.1; PID:
A;Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
submitted to the Protein Sequence Database, December 1990
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Fi102-1079/Domain: fibronectin type III repeat homology <FN3H-
Fi125-1275/Domain: (or 1259-1275) transmembrane #status predicted <TMM>
Fi126-1896/Domain: intracellular #status predicted <INT>
Fi126-1896/Domain: protein-tyrosine-phosphatase homology <PTP1>
Fi166-1897/Domain: protein-tyrosine-phosphatase homology <PTP1>
Fi165-1876/Domain: protein-tyrosine-phosphatase homology <PTP2>
Fi54-107,156-207,253-298/Disulfide bonds: #status predicted
Fi17,250,295,721,957/Binding site: carbohydrate (Aan) (covalent) #status pre
Fi153/Active site: Cys (phosphocysteine intermediate) #status predicted
Fi185/Binding site: Cys (phosphocysteine intermediate) #status predicted
Fi1830/Active site: Cys (phosphocysteine intermediate) #status predicted
Fi1830/Active site: Cys (phosphocysteine intermediate) #status predicted
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NiAlternate names: contactin; hexabrachion
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: JQ1325; A37936; B37936; S14571; S50209
R;Saga, Y:; Tsukamoto, T:; Jing, N.; Kusakabe, M.; Sakakura, T.
Gene 104, 177-185, 1991
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37.1%; Pred. No. 0.0065;
iive 10; Mismatches 35; Indels 11; Gaps
A;Reference number: S23126; MUID:92287069; PMID:1599438
A;Accession: S23252
A;Status: nucleic acid sequence not shown
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33; Conservative 1
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Best Local Similarity
Matches 33; Conserv
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A; Accession: A31930
A; Residues: 1-933 -400A
A; Residues: 1-933 -400A
A; Residues: 1-933 -400A
A; Cross-references: UNIPROT:P10039; UNIPARC:UP10000177AF5
A; Note: the authors' translation of the codons for residues 601-620 differs considerably C; Superfamily: tensecin; EGF homology; fibrinogen beta/gamma homology; fibronectin type C; Keywords: alternative splicing; glycoprotein
F; 13-39 / Domain: EGF homology < EGFS
F; 13-4-215 / Domain: fibronectin type III repeat homology < FN3A>
F; 215-39 / Domain: fibronectin type III repeat homology < FN3D>
F; 407-491 / Domain: fibronectin type III repeat homology < FN3D>
F; 409-576 / Domain: fibronectin type III repeat homology < FN3D>
F; 587-68 / Domain: fibronectin type III repeat homology < FN3D>
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F; 860-933 / Domain: fibronectin type III repeat homology (fragment) < FN3G>
F; 860-933 / Domain: fibronectin type III repeat homology (fragment) < FN3G>
F; 860-933 / Domain: fibronectin type III repeat homology (fragment) < FN3G>
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F; 860-933 / Domain: fibronectin type III repeat homology (fragment) < FN3G>
F
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R;Jones, F.S.; Burgoon, M.P.; Hoffman, S.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.M. Proc. Natl. Acad. Sci. US.A. 85, 2186-2190, 1988
A;Title: A cDNA clone for cytotactin contains sequences similar to epidermal growth fact A;Reference number: A31930; MUID:88176910; PMID:2451243
RESULT 15
A31930
cytotactin - chicken (fragments)
C;Species: Gallus gallus (chicken)
C;Species: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.9%; Score 108; DB 2; Length 933; Best Local Similarity 33.7%; Pred. No. 0.0052; Matches 32; Conservative 13; Mismatches 42; Indels
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3 DVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPW---ASIATI 59

SGLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94

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Search completed: February 23, 2006, 07:48:17 Job time : 40 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

OM protein - protein search, using sw model

February 23, 2006, 07:40:29 ; Search time 228 Seconds (without alignments) 290.876 Million cell updates/sec Run on:

US-09-688-566-81

94 494 1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKYDDPISINYRT Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

.bs Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IAN Q59g22 homo sapien	Q6n084 homo	Omod 08m2s0 homo	Q68cx6 homo	Q585t2 homo	ошоч варвуб	Q60fe4 homo	Omod 6dp89D	Q6n0a6 homo	Q59ehl homo	Q68dt4 homo	P02751 homo	Q6n025 homo	Q6mzu5 homo	Q6mzm7 homo	P07589 bos	P11276 mus musculu	P04937	P11722	058x60	A Q91289 pleurodeles	A Q91740 xenopus lae	Q6gqa5	04 rnc4					Q28692 orycto	778870
ID	QSCZ99_HUMAN	Q59G22 HUMAN	Q6N084 HUMAN	Q6MZS0 HUMAN	Q68CX6 HUMAN	Q585T2 HUMAN		Q60FE4 HUMAN	Q68DP9 HUMAN	Q6N0A6 HUMAN	Q59EH1 HUMAN	Q68DT4 HUMAN	FINC HUMAN	Q6N025 HUMAN	Q6MZU5_HUMAN	Q6MZM7 HUMAN	FINC BOVIN	FINC MOUSE	FINC RAT	FINC CHICK	Q9XSGO RAB	FINC PLEWA	FINC XENLA	Q6GQA5 XEN	Q4RNC4 TETNG	Q501R6 XENTR	093406 BRARE	Q6JAN2_BRARE	Q58XP5_BRARE	Q28692 RABIT	PINC HORSE
DB	5	~	~	~	~	7	N	N	7	N	~	~	-	~	~	~	-	П	Н	Н	~	Н	н	~	N	N	N	N	~	7	,-
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* Query Match	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	72.1	71.7	67.4	67.4	63.0	54.5	53.4	53.0	53.0	51.4	51.4	50.8	49.8	49.8	31.0	2.5
Score	361	361	361	361	361	361	361	361	361	361	361	61	61	61	61	26		333	333	311	269	264	262	262	254	254	251	246	246	153	130
Result No.	-	8	m	4	2	9	7	80	0,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	

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035452 MOUSE 054796_MOUSE 054796_MOUSE 0595KV4 BOVIN 095KV5_BOVIN 095KV5_BOVIN 095KV5_BOVIN 077376_BRARE 077376_BRARE 058774_HUMAN 090K79_HUMAN TENX_HUMAN 090K76_HUMAN 090K76_HUMAN
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ostomi; Hominidi 15 B., Wiemann 8	0; Gaps	WASIAT	
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rte) rata; Bute ; Catarrhi ; Catarrhi da; Han M databases.	Length 787 ; Indels	FGGNS PV	
ated) t annotation update) t annotation update) t annotation update) 370 (Fragment). raniata; Vertebrat lires; Primates; C lires; Primates; C sanger A., Fobo G. L/GenBank/DDBJ dat mRNA. hydrog SB49003169158ADD C	DB 2; 1 2.4e-30; thes 17;	RITYGE          RITYGE  RT 94	1RT 330
787 uence otatic Fragme Fragme ; Prim ne; Rittmu r A., Bank/L g.	61; O. 2. atche	OSRYY      TVRYY 	ISINY
rreat rate of the reat	Score 361; Di Pred. No. 2.46 4; Mismatches	VSDVPRDLEVVAATPTSRLISWNRSGLOSRYYRITYGETGGNSPVQEFTVPPWASIATIS	ĠĹĸ₽ĠVĎŶŢĬŢVŶĀVŢGRGĎSPASSKPĬSĬŇŶŔŢ
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MANN  MAY-2005 (TERMELEE] 30,  MAT-2005 (TERME	Similarity 77.	PRDLE       PRDLE GVDYT	GVDYT
ANY  YE 2005 (TEE  XY 2005 (TEE  XY 2005 (TEE  XY 2005 (TEE  XY 2005 (TEE  YOUR SEGIN  TAXID = 9606;  TAXID = 960041;  TAXID = 960069;  TAXID	Simi 3;		-
17. 1 19. HUMAN  QEC299_HUMAN PRELIMINARY;  QEC299_HUMAN PRELIMINARY;  10.MAY-2005 (TrEMBLrel. 30, I  10.MAY-2005 (TrEMBLrel. 30, I  10.MAY-2005 (TrEMBLrel. 30, I  10.MAY-2005 (TrEMBLrel. 30, I  Hypothetical protein DKF2p686  Name-DKF2p68611370;  Eukaryota; Metazoa; Chordata;  Mammalia; Butheria; Buarchonte  NCBI_TaxID=9606;  [1]  NCBI_TaxID=9606;  [1]  NUCLEOTIDE SEQUENCE.  TISSUE=Endometrium carcinoma  The German CDNA Consortium;  Mewes H.W. Weil B., Amid C.,  Submitted (FEB-2025) to the E  EMBL; CR93662; CAIE5766.1;  InterPro; IPR003962; PAIII su  InterPro; IPR003962; PAIII su  InterPro; IPR003962; PAIII su  InterPro; IPR003962; PAIII su  InterPro; IPR003961; FN III  PEAM; SPR00041; FN INTYPEIII.  PROSITE; PSS00687; ALDEHYDE DB  PROSITE TRESTOR PROSITE	atc ca]	1 237 61	297
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PRT; 1011 AA. RESULT 2
OS9G22_HUMAN
D59G22_HUMAN PRELIMINARY;
AC OS9G22;
DT 10-MAY-2005 (TEMBLE1. 30, C2)
DT 10-MAY-2005 (TEMBLE1. 30, L5)
DT 10-MAY-2005 (TEMBLE1. 30, L6)
DT 10-MAY-2005 (TEMBLE1. 30, L6)

Created) Last sequence update) Last annotation update)

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Query Match
Best Local Similarity 77.7*
Short 13; Conservative
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QEMZSO;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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TIGSUE-Human colon endothel primary cell culture;
The German Human cDNA Consortium;
The German Human cDNA Consortium;
The German Human cDNA Consortium;
A FODD G., Han M., Wiemann S.,
I Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; BX640638; CAE45786.1; -; mRNA.
SWR; Q6N044; 1-309, 402-601; -; mRNA.
SWR; Q6N044; 1-309, 402-601; -; mRNA.
R InterPro; IPR002086; Aldehyd dehydrog.
R InterPro; IPR00396; Aldehyd dehydrog.
R InterPro; IPR003962; FnIII subd.
R InterPro; IPR003961; FNIII subd.
R EMBL; PF00039; fn1; 3.
R Pfam; PF00041; fn3; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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"None Tile.";
Submitted (Mar-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AB209287; BAD92524.1; -; mRNA.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686Lill144 (Fragment).
Name-DKFZp686Lill44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SMO0058; FN1; 3.
SMART; SMO0060; FN3; 8.
PROSITE; PS00067; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS01253; FIBRONECTIN_1; 3.
PROSITE; PS50853; FN3; 9.
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Fibronectin 1 variant (Fragment).
                                  Name=Fibronectin 1 variant;
Homo sapiens (Human).
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PRINTS; PR00014; FNTYPEIII.
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Q6N084;
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TISSUB-Human uterus endothel primary cell culture;
TISSUB-Human uterus endothel primary cell culture;
The German Human cDNA Consortium;
The Man M., Wiemann S.;
Submitted (AuG-2003) to the EMBL/GenBank/DDBJ databases.
The EMBL; BX640920; CAE45958.1; -; mRNA.
The EMBL; BX640920; CAE45958.1; -; mRNA.
The Proc.; IPR002096; Aldehyd dehydrog.
The The Proc.; IPR002096; Falike.
The The Proc.; IPR003962; Falixe.
The Proc.; IPR003962; Falixe.
The Proc.; IPR003962; Falixe.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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73.1%; Score 361; DB 2; Length 1034; 77.7%; Pred. No. 3.3e-30; ive 4; Mismatches 17; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686022169 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO0687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
PROSITE; PSO0022; EGF 1; UNKNOWN 1.
PROSITE; PS01253; FIBRONECTIN_1; 3.
PROSITE; PS50853; FN3; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 GLKPGVDYTITVXAVTGRGDSPASSKPISINYRT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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ACCOCC OSSINATION OF THE PROPERTY OF THE PROPE

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WUCLEOTIDE SEQUENCE.

RG TISSUE-Amygdala;

RG The German CORA CORSORTIUM;

RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RESULT CAHHSITOLI: - imRA.

RESULT CAHHSITOLI: - imRA.

ROS GO: 00016491; Froxidoreductase activity; IEA.

ROS GO: 00016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.1%; Score 361; DB 2; Length 2217; Best Local Similarity 77.7%; Pred. No. 8.3e-30; Matches 73; Conservative 4; Mismatches 17; Indels (
                                                                                                                                                                              Wilson R.K.; Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases. Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AC012462; AAX76513.1; -; Genomic_DNA. Hypothetical protean. Now TER 2217 2217 SEQUENCE 2217 AA; 243438 MW; FAF1D07FBB6C44E5 CRC64;
                                             Waterston R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686H0342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1507 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 1540
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SMART; SM00059; FN1, 12.
SMART; SM00069; FN2; 2.
FRART; SM00060; FN3; 15.
PROSITE; PS000687; ALDEHYDE_DEHYDR_GLU; 1.
PROSITE; PS01022; EGF 1; 2.
PROSITE; PS01023; FN1_1; 10.
PROSITE; PS01021; FN1_2; 10.
PROSITE; PS01023; FN2_1; 2.
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PRINTS; PR00013; FNTYPEII.
PRINTS; PR00014; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEBDPB_HUMAN PRELIMINARY;
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Pfam; PF00040; fn2; 2.
Pfam; PF00041; fn3; 15.
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NUCLEOTIDE SEQUENCE
                                                                                                                                                   NUCLEOTIDE SEQUENCE
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ID QGBDBB HI

OGBDBB HI

DT 25-OCT-2(
DT 25-OCT-2(
DT 25-OCT-2(
DE HYPOCHETS)

OC HOMO SAPPOCHETS

OX NCBL TAX.

RN NTCLEOTIL

RC HOMO SAPPOCHETS

OX NCBL TAX.

RN NUCLEOTIL

RC TISSUB-AHA

RA MEWES HI

DR SMR1, GR

DR PETER

DR 
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           STWREARTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Pobo G., Han M., Wiemann S.;

Submitted (Aud-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR749666; CAH18457.1; -; mCNA.

SMR; Q68CX6; 1-226, 349-441-709, 1061-1331.

GO; GO:0001576; C:extracellular region; IEA.

GO; GO:0001576; C:extracellular region; IEA.

GO; GO:000152; P:extadoreductase activity; IEA.

InterPro; IPR002086; Aldehyd_dehydrog.

R InterPro; IPR003962; PIII embd.

InterPro; IPR003962; PIII embd.

InterPro; IPR003962; PIII embd.

R Pfam; PF00013; FNTYPEII.

R Pfam; PF00014; FNTYPEII.

R PRINTS; RR00014; FNTYPEII.

R PRINTS; RR00016; FNIYPEII.

SMART; SM00060; FNI; 6.

SMART; SM00060; FNI; 6.

R PROSITE; PS00022; EGF 1; 6.

R PROSITE; PS001253; FIBRONECTIN_1; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 361; DB 2; Length 214
Pred. No. 8e-30;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2146 AA; 235425 MW; D526ABD713C571DE CRC64;
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                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686013149.
Name-DKFZp686013149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein FNI (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Colon endothel;
The German cDNA Consortium;
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Q585T2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 2146 AA;
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NUCLEOTIDE SEQUENCE
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ID QENOAE HU

AC QENOAE;

DT 05-JUL-20

DT 05-JUL-20

DT 05-JUL-20
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Matches
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                            1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
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                                                                                              Score 361; DB 2; Length 2240;
Pred. No. 8.4e-30;
4; Mismatches 17; Indels
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PROSITE; PS51092; FN2_2; 2.
PROSITE; PS50853; FN3; 15.
Hypochetical protein; Repeat.
SEQUENCE 2240 Aa; 246668 MW; 8FCDAF406F330621 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2265 AA; 249411 MW; 74A67590564C28AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fram, FF00041; fin3; 15.

PRINTS; PR00041; FNTYPEI.

PRINTS; PR00012; FNTYPEI.

PRINTS; PR00013; FNTYPEII.

PRODON; PR00014; FNTYPEIII.

ProDON; PR00059; FN TYPEIII.

SMART; SM00059; FN TYPEIII.

SMART; SM00060; FN3; 12.

SMART; SM00060; FN3; 12.

PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.

PROSITE; PS01253; FNENGNETIN 1; 12.

PROSITE; PS01253; FNENGNETIN 2; 2.

PROSITE; PS0183; FN3; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                             1507 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 1540
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                                                                                                                                                                                                                                                                                                                                                                                         2265 AA
                                                                                                73.1%;
77.7%;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                          Query Match
Best Local Similarity 77.,
73, Conservative
                                                                                                                                                                                                                                                                                                                                                                                     QEOFE4 HUMAN PRELIMINARY;
QEOFE4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibronectin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=FN1
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Charles and Consortium;

Charles E. Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,

Robb G., Han M., Wiemann S.;

Robb G., Han M., Wiemann S.;

Built CR149316; CAH181711; -; mRNA.

CO; GO:0005576; C:extracellular region; IEA.

CO; GO:0016491; F:oxidoreductase activity; IEA.

CO; GO:0016491; F:oxidoreductase activity; IEA.

Robbert C. PRR002086; Aldehyd dehydrog.

R InterPro; IPR0002081; Fibrnctn1.

R InterPro; IPR0003086; Ribrnctn1.

R InterPro; IPR0003081; Fibrnctn1.

R InterPro; IPR000396; FM III.

R Fam; PR000041; fn1; 12.

R PRINTS; RR00013; fn1; 12.

R PRINTS; RR00014; FNTYPEII.

R PRINTS; RR000195; FNTYPEII.

R PRINTS; RR000195; FNTYPEII.

R SMART; SM00059; FNT; 12.

R SMART; SM00059; FNT; 12.

R SMART; SM00059; FNT; 13.

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PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01223; FN1 1; 12.
PROSITE; PS00023; FN2 1; 12.
PROSITE; PS00023; FN2 1; 2.
PROSITE; PS51092; FN2 2; 2.
PROSITE; PS51092; FN2 2; 2.
PROSITE; PS51092; FN3 2; 3.
PROSITE; PS51092; FN3 2; 4.
PROSITE; PS51092; FN3 5; 4.
PROSITE; PS51092; FN3 5; 4.
PROSITE; PS51092; FN3 5; 4.
PROSITE; PS51093; FN3 5; 4.
PROSITE; F
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                               Last sequence update)
Last annotation update)
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      PRT; 2267 AA
                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
Hypothetical protein DKFZp666K08164.
Name=DKFZp686K08164;
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QGNOA6;
Q68DP9_HUMAN PRELIMINARY;
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AB209840; BAD93077.1; -; mRNA. NON TER 1
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SWART; SM00059; FN1; 12.
SWART; SM00069; FN1; 12.
SWART; SW00060; FN3; 15.
PROSITE; PS000687; ALDEHYDE DEHYDR_GL;
PROSITE; PS00022; FN2 12.
PROSITE; PS00023; FN2 1; 12.
PROSITE; PS51092; FN2 1; 2.
PROSITE; PS51092; FN2 1; 2.
PROSITE; PS51092; FN2 1; 2.
PROSITE; PS5093; FN3 15.
HYDOThetical protein; Repeat.
SEQUENCE 2357 AA; 259092 MW; BEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-0CT-2004 (TrEMBLrel. 28, Created) 25-0CT-2004 (TrEMBLrel. 28, Last seq 25-0CT-2004 (TrEMBLrel. 28, Last ann Hypothetical protein DKFZp686F10164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Uterus endothel;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0012; FNTYPEI.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00014; FNTYPEIII
                                                                                                                                                                           Best Local Similarity 77.74
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q68DT4 HUMAN PRELIMINARY;
Q68DT4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=DKFZp686F10164;
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                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                           Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                           Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BK640608; CAE45714.1; "RNA.

GO; GO:0005576; C:extracellular region; IEA.

InterPro; IPR002086; Aldehyd_dehydrog.

InterPro; IPR000083; Fibrnctnl.

InterPro; IPR003962; FinII subd.

InterPro; IPR003962; FNIII subd.

InterPro; IPR003962; FNIII subd.

InterPro; IPR003962; FNIII subd.

InterPro; IPR003652; FNIII subd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 2296 AA; 252761 MW; 9AB2D723CCOCED70 CRC64;
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PRINTS; PRO0013; FNTYPEII.
PRINTS; PRO0014; FNTYPEII.
PRODOM; PD000995; FN Type_II; 2.
SMART; SM00059; FN2; 2.
SMART; SM00069; FN2; 2.
SMART; SM00060; FN3; 15.
PROSITE; PS00067; ALDEHYDE DEHYDR GLU; UNKNOWN_I.
PROSITE; PS00022; EGF 1; UNKNOWN_Z.
PROSITE; PS01253; FIBRONECTIN_I; 12.
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Q59EH1;
10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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  Hypothetical protein DKF2p686M04163.
Name=DKF2p686M04163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01253; FIBKONECLIN_2; 2. PROSITE; PS00023; FIBRONECTIN_2; 2. PROSITE; PS50853; FN3; 15.
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The German cDNA Consortium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 77.7
nes 73; Conservative
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Pfam; PF00040; fn2; 2.
Pfam; PF00041; fn3; 15.
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                                                                    Homo sapiens (Human)
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                                                                                                                                                                                 NCBI_TaxID=9606;
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0559EH HUM
10 059EH AC
059EH DT 10-MA
DT 10-MA
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1533 VSDVPRDLEVVAATPISLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 1592
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                 Length 2351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FODO G., Han M., Wiemann S., Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

R GDJ GO:000576; C:extracellular region, IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R InterPro; IPR000206; Aldehyd dehydrog.

R InterPro; IPR000208; Aldehyd dehydrog.

R InterPro; IPR00081; Fibrnctn1.

R InterPro; IPR000852; FN LIII.

R InterPro; IPR000391; FN LIII.

R Pfam; PF00040; fn1; 12.

R Pfam; PF00041; fn3; 15.
                                                                 73.1%; Score 361; DB 2; Length 23 77.7%; Pred. No. 8.9e-30; ive 4; Mismatches 17; Indels
SEQUENCE 2351 AA; 258611 MW; 67149C626199075E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2357 AA
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domain.";
  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLECTIDE SEQUENCE OF 1-49.
MEDLINE=87175578; PubMed=3031656;
Dean D.C., Bowlus C.L., Bourgeois S.;
"Cloning and analysis of the promotor region of the human fibronectin
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Calaycay J., Pande H., Lee T., Borsi L., Siri A., Shively J.E.,
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                                                                                                                                                                                                    annotation update)
(Cold-insoluble globulin) (CIG)
                                                                                                                                                                                                                                                                                                                                                                                                                              The German cDNA consortium;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                FIGURE 1 PRT, 2186 AA. PRT, 2186 AA. P02751, 095609, 095610, 014312; 014325; 014326; (081V18; 096KP7; 096KP8; 096KP9; 09H188; 09HAP3; (21-JUL-1996 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Fibronectin precursor (FN) (Cold-insoluble globu Name-FN1; Synonymas-FN;
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                                                 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT
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MEDLINE=82255604; PubMed=7050098;
Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
"The cell attachment domain of fibronectin. Determination of the
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differing by an internal segment coding for a structural domain.";
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NUCLEOTIDE SEQUENCE OF 973-2386 (ISOPORM 3).
MEDLINE=84272258; PubMed=6462919;
MCOTALINELA A.R., Vibe-Pedersen K., Baralle F.E.;
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MEDLINE-88029324; PubMed-282287;
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MEDLINE=88041070; PUMPAGE=3478690;
MEDLINE=88041070; PUMPAGE=3478690;
MEDLINE=88041070; PUMPAGE=3478690;
"Identification of a third region of cell-spec
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J. Biol. Chem. 257:9593-9597(1982)
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MEDLINE=83290929; Pubmed=6688418;
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MEDLINE=86111901; Pubmed=3003095;
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Biochemistry 24:2698-2704(1985).
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J. Biol. Chem. 258:12670-12674(1983)
                                                MEDLINE=87026578; PubMed=3021206;
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PubMed=6304699;
                       NUCLEOTIDE SEQUENCE OF 1712-1739
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G., Han M., Wiemann S.;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence upd
05-JUL-2004 (TrEMBLrel. 27, Last annotation u
Hypothetical protein DKFZp686M2451 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE=Human endometrium carcinoma cell line;
                                                                                                                                                                                                                                                                                                     2444 AA
61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT
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SWART; SN00058; FN1; 12.
SWART; SN00059; FN2; 2.
SWART; SN00059; FN2; 2.
FN2; 2.
FN2; SWART; SN00059; FN2; 2.
FN3; 16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0012; FNTYPEI.
PRINTS; PRO0013; FNTYPEII.
PRINTS; PRO0014; FNTYPEIII
                                                                                                                                                                                                                                                                                                 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEMZUS_HUMAN PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=DKF2p686M2451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                    RC TISSUE-Endometrium carcinoma cell line;

RC TISSUE-Endometrium carcinoma cell line;

RG THE German CDNA CONSOTTIUM;

RA Bloccker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

RA Bloccker H., Eoch G., Han M., Wiemann S.;

RL BLICK, RSGOOS G., Han M., Wiemann S.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

REMBL, BX640875; CARSA532.1; -; mRNA.

GO; GO:0005576; C:extracellular region; IEA.

BRINGS INTERPRO; IPR002086; Aldehyd dehydrog.

RICK-PRO; IPR003962; FNIII sund.

BRINGS INTERPRO; IPR003962; FNIII sund.

BRINGS PR00040; FNIII.

BRENTS; PR00041; FNIYPEII.

BRENTS; PR00013; FNYTPEII.

BRENTS; PR00014; FNYTPEII.

BRENTS; PR00014; FNYTPEII.

BRENTS; RR00058; FNI; 12.

BRENTS; RR00058; FNI; 12.

BRENTS; RR00058; FNI; 12.

BRENTS; SNO0058; FNI; 12.

BRENTS; SNO0058; FNI; 12.

BRENTS; SNO0058; FNI; 12.

BRENTS; SNO0058; FNI; 12.

BRENTS; PS00023; FNIZYPEIII.

BRENTS; PS00023; FNIZYPEIII.

BRENTS; PS00023; FNIZYPEII.

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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                      Hypothetical protein DKFZp68601166.
Name=DKFZp68601166;
Homo sapiens (Human).
                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                         NCBI_TaxID=9606;
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Thu Feb 23 12:32:27 2006

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	
version - 2006	-
GenCore version 5.1.7 (c) 1993 - 2006 Biocce	•
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OM protein - protein search, using sw model

February 23, 2006, 07:40:25 Run on:

; Search time 186 Seconds (without alignments) 222.052 Million cell updates/sec

US-09-688-566-81

494 1 VSDVPRDLEVVAATPTSRLI.....VTDKSDTYKYDDPISINYRT 94 Title: Perfect score:

**BLOSUM62** Scoring table:

Sequence:

2443163 seqs, 439378781 residues Searched:

Gapop 10.0 , Gapext 0.5

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Genesed Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

#### SUMMARIES

	Description	D78898 Tum	Abb78921 Tumour ne	Abb78939 Tumour ne	Abb78919 Tumour ne	Abb78920 Tumour ne	Abb78911 Tumour ne	Abb78915 Tumour ne	Abb78940 Tumour ne	Abb78912 Tumour ne	Abb78916 Tumour ne	Abb78918 Tumour ne	Abb78899 Tumour ne	Abb78917 Tumour ne	Abb78922 Tumour ne	Abb78923 Tumour ne	Abb78949 Tumour ne	Abb78873 Tumour ne	Abb78869 Tumour ne	Abb78868 Tumour ne	Abb78872 Tumour ne	Abb78942 Tumour ne	Abb78870 Tumour ne	Abb78900 Tumour ne	Abb78871 Tumour ne
SUMMARIES	CI.	ABB78898	ABB78921	ABB78939	ABB78919	ABB78920	ABB78911	ABB78915	ABB78940	ABB78912	ABB78916	ABB78918	ABB78899	ABB78917	ABB78922	ABB78923	ABB78949	ABB78873	ABB78869	ABB78868	ABB78872	ABB78942	ABB78870	ABB78900	ABB78871
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٠	Query Match	100.0	100.0	99.0	99.0	0.66	98.8	98.4	0.86	0.86	97.8	97.8	97.4	96.8	93.7	90.3	89.7	88.9	88.6	88.5	87.2	84.8	84.4	84.2	84.0
	Score	494	494	489	489	489	488	486	484	484	483	483	481	478	463	446	443	439	437.5	437	431	419	417	416	415
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Abb78895 Tumour ne	Abb78941 Tumour ne	Abb78901 Tumour ne	Abb78897 Tumour ne	Abb78880 Tumour ne	Abb78879 Tumour ne	Abb78928 Tumour ne	Abb78954 Tumour ne	Abb78910 Tumour ne	Abb78881 Tumour ne	Abb78909 Tumour ne	Abb78950 Tumour ne	Abb78876 Tumour ne	Abb78896 Tumour ne	Abb78864 Tumour ne	Abb78867 Tumour ne	Abb78904 Tumour ne	Abb78878 Tumour ne	Abb78877 Tumour ne	Abb78866 Tumour ne	Abb78929 Tumour ne	
5 ABB78895	5 ABB78941	5 ABB78901	5 ABB78897	5 ABB78880	5 ABB78879	5 ABB78928	5 ABB78954	5 ABB78910	5 ABB78881	5 ABB78909	5 ABB78950	5 ABB78876	5 ABB78896	5 ABB78864	5 ABB78867	5 ABB78904	5 ABB78878	5 ABB78877	5 ABB78866	5 ABB78929	
94	94	94	16	94	94	94	94	94	46	94	94	94	93	94	94	94	93	94	94	94	
82.2	81.4	80.4	80.0	79.6	79.4	79.4	78.9	78.9	78.7	78.7	78.5	78.5	78.4	77.9	77.7	77.7	77.4	77.3	76.9	75.7	
406	402	397	395	393	392	392	390	390	389	389	388	388	387.5	385	384	384	382.5	382	380	374	
25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	1

## ALIGNMENTS

ABB78898 standard; peptide; 94 AA. (first entry) 30-JUL-2002 ABB78898; RESULT 1 ABB78898 

Tumour necrosis factor-alpha binding amino acid sequence T10.06.

Protein scaffold, antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Synthetic.

WO200232925-A2.

25-APR-2002.

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566.

(PHYL-) PHYLOS INC.

Kuimelis RG; Wagner RW, Lipovsek D,

WPI; 2002-444238/47.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest.

Claim 47; Fig 25; 94pp; English.

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel

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proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and colded in prokaryotic systems (e.g. Bacherichia coll), in eukaryotic systems (e.g. Pacherichia coll), in eukaryotic systems (e.g. pacherichia coll), in eukaryotic systems (e.g. yeast), or in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention
   binding proteins useful in the above-mentioned fields. The present
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Sequence 94 AA;

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                                                                     1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGRTGGNSPVQEFTVPPWASIATIS
                               0; Gaps
100.0%; Score 494; DB 5; Length 94; 100.0%; Pred. No. 1.2e-49;
                            Indels
                             .
                                                                                                                             61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                            61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                            0; Mismatches
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RESULT 2

ABB78921 standard; peptide; 94 AA ABB78921; Tumour necrosis factor-alpha binding amino acid sequence T14.26.

(first entry)

30-JUL-2002

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework. 

Homo sapiens

WO200232925-A2 Synthetic.

25-APR-2002

16-OCT-2001; 2001WO-US032233

16-OCT-2000; 2000US-00688566

(PHYL-) PHYLOS INC.

Kuimelis RG; Wagner RW, Lipovsek D,

WPI; 2002-444238/47.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen

Claim 47; Fig 25; 94pp; English.

domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of The present invention describes a non-antibody protein, comprising a

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nM to a compound that is

Claim 47; Fig 25; 94pp; English.

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interest, or for destroying or inactivating antibody molecules. The nonautibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and concentrations. In addition, these molecules are readily expressed and concentrations. In addition, these molecules are readily expressed and concentrations in addition, these molecules are exacting systems (e.g. reability maturation techniques involving multiple cycles of smenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein scaffold, antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.
                                                                                                                                                                                                                                                                                                                                                         Length 94;
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                                                                                                                                                                                                                                                                                                                                                        Score 494; DB 5;
Pred. No. 1.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLKPGVDYTITVYAVTDKSDTYKYDDFISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        100.0%;
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At; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-444238/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PHYL-) PHYLOS INC.
                                                                                                                                                                                                                                                                                                                     Sequence 94 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
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is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. peast), or in in vitro translation systems (e.g. rabbit menable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection sing multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention
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Sequence 94 AA;

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                                                          1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
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Score 489; DB 5; Length 94;
Pred. No. 4.4e-49;
2; Mismatches 0; Indels
                                                                                        GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                      92; Conservative
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  Query Match
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ABB78919 standard; peptide; 94 AA 30-JUL-2002 ABB78919; 

Tumour necrosis factor-alpha binding amino acid sequence T14.14. (first entry)

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens

Synthetic.

WO200232925-A2

25-APR-2002.

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566

(PHYL-) PHYLOS INC.

Kuimelis RG; Wagner RW, Lipovsek D,

WPI; 2002-444238/47.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen

Claim 47; Fig 25; 94pp; English.

The present invention describes a non-antibody protein, comprising

domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that not bound as tightly by the reference protein. The non-antibody protein is useful as scaffelols for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antign of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fitalds, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely senable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the present invention the exemplification of

Sequence 94 AA;

1 VSDVPRDLEVVAATPISKLISWNRSGLQSRYYRITYGETGGRSPVQEFTVPPWASIATIS 60 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60 Gaps ö Length 94; Indels 99.0%; Score 489; DB 5; 98.9%; Pred. No. 4.4e-49; iive 0; Mismatches 1. 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 93; Conservative Local Similarity Query Match Best Loc Matches 셤 8 ò

GLKPGVDYTITVYAVTDKSDTYKYDDPTSINYRT 94

셤

ABB78920 standard; peptide; 94 AA ABB78920;

30-JUL-2002 (first entry)

Tumour necrosis factor-alpha binding amino acid sequence T14.23.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens.

Synthetic.

WO200232925-A2

25-APR-2002

X4X4X4X4X4X4X6X4X6XX4X6X4X4X4444444

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566

(PHYL-) PHYLOS INC.

Kuimelis RG; Lipovsek D, Wagner RW,

WPI; 2002-444238/47.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen interest

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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins by an evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and colded in prokaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Purthermore, these proteins are extremely amended to a ffinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using multiple cycles of selection, e.g. in vitro selection using multiple protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention
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Pred. No. 4.4e-49;
0; Mismatches 1; Indels
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Claim 47; Fig 25; 94pp; English.
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nes 93; Conservative
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protein having an interminated could sequence, where the non-antibody protein having an untated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present corteins have thermodynamic properties superior to those of natural antibody mimics exhibit improved biophysical properties, such as antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as extremely concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia existems (e.g. readily or yeast system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of the exemplification of the present invention
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designing proteins with specific properties, e.g. for binding any antigen
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                                                                                                            The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.9%; Score 488; DB 5; 98.9%; Pred. No. 5.8e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB78915 standard; peptide; 94 AA.
                                                               Claim 47; Fig 25; 94pp; English.
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es 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 94 AA;
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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nm to a compound that is not bound as tightly by the reference protein. The non-antibody protein is acaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins useful in the above-mentioned fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins or antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing condition, these molecules are readily expressed and colded in prokaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. yeast), or in in vitro translation systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amendable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen Claim 47; Fig 25; 94pp; English. 

Sequence 94 AA;

ó 9 9 VSDVPRDLEVVAATPTSRLISWNRSGLOSRYYRITYGETGGNSPVOEFTVPPWASIATIS 1 LSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIAAIS 0; Gaps DB 5; Length 94; 1; Indels GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 Score 486; DB 5. Pred. No. 1e-48; 1; Mismatches 98.4%; Query Match
Best Local Similarity 97.3.
Best Local Similarity 97.3.
Gonservative a 셤 ò ð

ABB78940 standard; peptide; 94 AA 30-JUL-2002 ABB78940; ABB78940 RESULT 

(first entry)

Tumour necrosis factor-alpha binding amino acid sequence M12.01.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens Synthetic. WO200232925-A2

25-APR-2002.

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566.

(PHYL-) PHYLOS INC.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia coll), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention Kuimelis RG; Claim 47; Fig 25; 94pp; English. Wagner RW, WPI; 2002-444238/47. Lipovsek D, of interest 

Sequence 94 AA;

1 VSDVPRDLEVVAATPISRLISWNRSGLOSRYYRITYGETGGNSPVQEFTVPPWASIATIS Gaps ö Length 94; Indels Match 98.0%; Score 484; DB 5; Local Similarity 96.8%; Pred. No. 1.7e-48; les 91; Conservative 2; Mismatches 1. Query Match Best Loc Matches

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61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 GIKPGVDYTIIVYAVTDESDTYKYDDPVSTNYRT 94 셤

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RESULT 9 ABB78912 ABB78912 standard; peptide; 94 AA ABB78912; 

30-JUL-2002 (first entry)

Tumour necrosis factor-alpha binding amino acid sequence S08.03.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens. Synthetic.

WO200232925-A2

25-APR-2002

16-OCT-2001; 2001WO-US032233

16-OCT-2000; 2000US-00688566

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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mW to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibody maincs exhibit improved biophysical properties, such as antibody maincs exhibit improved biophysical properties, such as attibody minics exhibit improved biophysical properties, such as attibody minics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and colded in prokaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amended of finity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                              New non-antibody proteins having an immunoglobulin fold, useful in
research, therapeutic or diagnostic fields, particularly as scaffolds for
designing proteins with specific properties, e.g. for binding any antigen
of interest.
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                                                                                   Lipovsek D, Wagner RW,
                                                                                                                                        WPI; 2002-444238/47
                          (PHYL-) PHYLOS INC.
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Sequence 94 AA;

9 9 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 1 VSDVPRDLEVVAATPISRLISWNRSGLOSRYYRITYGETGGNGPVQEFTVPPWASIATIS . 0 Score 484; DB 5; Length 94; Pred. No. 1.7e-48; 2; Indels 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 GLKPGVDYTITVYAVTDMSDTYKYDDPISINYRT 94 0; Mismatches 98.0%; 92; Conservative Query Match Best Local Similarity tches 셤 Š

RESULT 10

ABB78916 standard; peptide; 94 AA ABB78916; 

Tumour necrosis factor-alpha binding amino acid sequence T14.13.

30-JUL-2002 (first entry)

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens Synthetic. WO200232925-A2

25-APR-2002,

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566.

(PHYL-) PHYLOS INC

Kuimelis RG;

Kuimelis RG; Wagner RW, Lipovsek D,

WPI; 2002-444238/47.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest

Claim 47; Fig 25; 94pp; English.

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference of protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibody mimics exhibit improved hophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and consent antibody minimals. folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention

Sequence 94 AA;

0; Gaps Length 94; 1; Indels 97.8%; Score 483; DB 5; 97.9%; Pred. No. 2.2e-48; 97.9%; Pred. No. 2.26 ive 1; Mismatches Best Local Similarity 97.9 Matches 92; Conservative Query Match

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1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQELTVPPWASIATIS 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS

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ABB78918 standard; peptide; 94 AA. RESULT 11 ABB78918

ABB78918;

(first entry) 30-JUL-2002 BXSSXXXXXXXXXXXXX

Tumour necrosis factor-alpha binding amino acid seguence T14.05.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

sapiens. Synthetic WO200232925-A2

us-09-688-566-81.rag

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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mW to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fitelds, and for screening novel binding proteins useful in the above-mentioned fitelds. The present proteins have thermodynamic properties superior to those of natural antibody mimics exhibit improved biophysical properties, such as concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic systems (e.g. Escherichia coli), in eukaryotic reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of salection, e.g. in vitro selection using RNA-protein fusion technology, changed display systems. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                      New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen
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                                                                                                                                                                                                                                   Kuimelis RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 47; Fig 25; 94pp; English
                                                                            16-OCT-2001; 2001WO-US032233.
                                                                                                                              16-OCT-2000; 2000US-00688566
                                                                                                                                                                                                                                      Wagner RW,
                                                                                                                                                                                                                                                                                     WPI; 2002-444238/47
                                                                                                                                                                                  (PHYL-) PHYLOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 94 AA;
                                                                                                                                                                                                                                   Lipovsek D,
                           25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                         of interest
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Kuimelis RG;

Lipovsek D, Wagner RW, WPI; 2002-444238/47

(PHYL-) PHYLOS INC.

16-OCT-2001; 2001WO-US032233 16-OCT-2000; 2000US-00688566

WO200232925-A2.

Synthetic.

25-APR-2002

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                                                                           1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRIIYGETEGNSPVQEFTVPPWASMAIIS
                                                             VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                 Gaps
                                 ö
    Length 94;
                              1; Indels
 97.8%; Score 483; DB 5;
97.9%; Pred. No. 2.2e-48;
tive 1; Mismatches 1;
                                                                                                                      94
                                                                                                                                     61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT
Query Match
Best Local Similarity 97.9
Matches 92; Conservative
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Tumour necrosis factor-alpha binding amino acid sequence T10.17.
              ABB78899 standard; peptide; 94 AA.
                                         (first entry)
                                          30-JUL-2002
                           ABB78899;
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Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Ното варіеля

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New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia coll), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely smenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein scaffold; antibody; binding protein; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 481; DB 5;
Pred. No. 3.8e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phage display or yeast display systems. The presemblification of the present invention
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 47; Fig 25; 94pp; English
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98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB78917 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 94 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           interest
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Matches
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Numour necrosis factor-alpha binding amino acid sequence T14.24

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New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen
tumour necrosis factor alpha; TNF-alpha; protein framework.
                                                                                                              Kuimelis RG;
                                                                                                                                                                                 Claim 47; Fig 25; 94pp; English
                                                                  16-OCT-2001; 2001WO-US032233
                                                                                16-OCT-2000; 2000US-00688566
                                                                                                              Lipovsek D, Wagner RW,
                                                                                                                             WPI; 2002-444238/47
                                                                                               (PHYL-) PHYLOS INC.
                                    WO200232925-A2
               Homo sapiens
                                                   25-APR-2002
                                                                                                                                                                    interest
                       Synthetic
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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, antibody protein is also useful in all areas where antibodies are used, antibody protein sueful in the above-mentioned fields. The present proteins useful in the above-mentioned fields. The present proteins by and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as artibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, the exemility or yeast display systems. The present sequence is used in the exemilation of the present income. phage display or yeast display systems. The the exemplification of the present invention

Sequence 94 AA;

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9
                                                                                                                                VSDVPRGLEVVAATPISRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                       1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                               Gapa
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96.8%; Score 478; DB 5; Length 94; 97.9%; Pred. No. 8.6e-48; ive 0; Mismatches 2; Indels
                                                                                                                                                                             61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                     61 GLKHGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                            92; Conservative
                    Best Local Similarity
    Query Match
                                               Matches
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ABB78922 standard; peptide; 94 AA (first entry) 30-JUL-2002 ABB78922; ABB78922

RESULT 14

ABB78923

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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated annion acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibody minics exhibit improved biophysical properties, such as antibodies, and can be evolved rapidly in vitro. The present proteins or antibody minics exhibit improved biophysical properties, such as catability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia are extremely reticulocyte lysate system). Furthermore, these proteins are extremely mentioned to affinity maturation techniques involving multiple cycles of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen
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                                      Protein scaffold, antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.
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Pred. No. 4.9e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                          Kuimelis RG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 47; Fig 25; 94pp; English.
                                                                                                                                                                                                                                                         16-OCT-2001; 2001WO-US032233.
                                                                                                                                                                                                                                                                                                    16-OCT-2000; 2000US-00688566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 93.7%;
| Similarity 93.6%;
88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Wagner RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-444238/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                               (PHYL-) PHYLOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 94 AA;
                                                                                                                                                                     WO200232925-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of interest.
                                                                                                                                                                                                                                                                                                                                                                                          Lipovsek D,
                                                                                                                                                                                                                25-APR-2002
                                                                                                                            Synthetic
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ABB78923
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(first entry)
30-JUL-2002
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Tumour necrosis factor-alpha binding amino acid sequence T14.20.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens

25-APR-2002

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566.

Kuimelis RG; Lipovsek D, Wagner RW,

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest.

Claim 47; Fig 25; 94pp; English.

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel pinding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as cability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and solubility under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and solubility maturation systems (e.g. reabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention

Sequence 94 AA;

0; Gaps 90.3%; Score 446; DB 5; Length 94; 91.5%; Pred. No. 4.8e-44; tive 1; Mismatches 7; Indels Local Similarity 91.5 ses 86; Conservative Query Match Best Loca Matches

1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60 1 VSDVPRDLEVVAATPTSRLISWRNIYPIARYYRITYGETGGNSPVQEFTVPPWASIATIS

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Search completed: February 23, 2006, 07:43:38 Job time : 187 secs

(PHYL-) PHYLOS INC. WO200232925-A2. Synthetic. 

WPI; 2002-444238/47

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GenCore version 5.1.7
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                    Copyright
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OM protein - protein search, using sw model

February 23, 2006, 07:47:49 Run on:

; Search time 47 Seconds (without alignments) 165.351 Million cell updates/sec

US-09-688-566-81

494 1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKYDDPISINYRT Perfect score: Sequence:

Scoring table:

572060 segs, 82675679 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:* Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SIMMARIES

	Description	Sequence 8, Appli	110	80	7	110,	112,	112,	112,	34, A	Sequence 34, Appl	34,	1,	10	12	3, 2	25	25,	Sequence 25, Appl	'n	11	Sequence 8, Appli	4,	13,	7,	'n		29,
SUMMARIES	ID	US-08-717-169-8	US-09-638-202A-110	US-09-228-901A-8	US-09-096-749A-110	US-09-637-614-110	US-09-638-202A-112	US-09-096-749A-112	US-09-637-614-112	US-08-078-683A-34	US-08-471-970A-34	US-09-723-677B-34	US-07-959-369-1	US-07-959-369-10	US-07-959-369-12	US-08-836-854-3	US-09-366-009-25	US-08-809-156B-25	US-09-775-964-25	US-07-959-369-3	US-07-959-369-11	US-08-836-854-8	US-07-959-369-4	US-07-959-369-13	US-08-836-854-7	US-08-836-854-5	US-09-366-009-29	US-08-809-156B-29
	80	П	~	~	7	7	N	α	~	Н	7	7	-	-	Н	Н	~	~	~	Н	Н	Н	Н	Н	Н	Н	7	7
	Query Match Length	94	94	94	94	94	96	96	96	175	175	175	256	258	274	274	274	274	. 274	277	279	279	281	283	283	302	302	302
de	Query	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1
	Score	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361
	Result No.	-	7	٣	4	S	9	7	80	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

302 2 US-09-775-964-29 332 1 US-08-836-854-13 367 1 US-08-836-854-14 367 1 US-08-836-854-14 368 1 US-08-836-854-17 388 1 US-07-959-369-5 385 1 US-07-959-369-5 385 1 US-07-959-369-10 432 1 US-07-959-369-9 432 1 US-08-836-854-12 432 1 US-08-836-854-20 433 1 US-08-836-854-20 434 1 US-08-836-854-20 435 2 US-09-366-009-4 446 1 US-08-899-1568-4 446 1 US-08-836-854-16 457 2 US-09-765-084-4	Sequence 29, Appl Sequence 11, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 16, Appl Sequence 10, Appl Sequence 10, Appl Sequence 16, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appli Sequence 16, Appl Sequence 16, Appl Sequence 16, Appli
	US-09-775-964-29 US-08-816-854-113 US-08-816-854-114 US-08-816-854-114 US-08-816-854-117 US-07-959-369-15 US-07-959-369-15 US-07-959-369-9 US-08-816-854-12 US-07-959-369-9 US-08-816-854-12 US-08-816-854-12 US-09-316-009-4 US-08-816-814-4 US-08-816-814-4 US-08-816-814-4 US-08-816-814-4 US-08-816-814-16 US-08-816-814-4 US-08-816-814-16 US-08-816-814-16 US-08-816-814-16
	0 0 0 0 H 0 8 M 0 M 0 M 0 M 0 M 0 M 0 M 0 M 0 M 0

### ALIGNMENTS

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,169
FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
ATTONEY/AGENT INPOMEMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/POCKET UNMERR: P-LJ 2017
TELECOMMULTATION INPORMATION:
TELECOMMULTATION INPORMATION:
TELEPHONE: (619) 535-9001 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS: , MOLECULE TYPE: peptide US-08-717-169-8 TYPE: amino acid STRANDEDNESS

73.1%; Score 361; DB 1; Length 94; 77.7%; Pred. No. 1.8e-35; 4; Mismatches Query Match 73.1 Best Local Similarity 77.7 Matches 73; Conservative

1 VSDVPRDLEVVAATPTSLLISWDAPAVIVRYYRIIYGETGGNSPVQEFTVPGSKSTATIS 60 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS ઠે g

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LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.1
Best Local Similarity 77.7
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
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                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-228-901A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: i
ORIGINAL SOURCE:
US-09-096-749A-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A. STREET: 121 South Eighth Street, Ste. 1600 CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.1%; Score 361; DB 2; Length 94; Best Local Similarity 77.7%; Pred. No. 1.8e-35; Matches 73; Conservative 4; Mismatches 17; Indels
                                                                                                                                                    RESULT 2
US-09-638-202A-110
i Sequence 110, Application US/09638202A
j Fatent No. 6462189
j GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
j TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
AnneRSSEE: Schwegman, Lundberg, Woessner & Klut
AnneRSSEE: Schwegman, Lundberg, Ste. 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AND STATE AND STA
                                     61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,202A
FILING DATE: 11.Aug-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
RAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 94 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-638-202A-110
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TITLE OF INVESTIGN: Ameliorating Cancer by Using Superfibronectin (CURRENT APLICATION WURSER: US/02/028, 901A

CURRENT APLICATION WURSER: US/02/028, 901A

CURRENT PLINE DATE: 2002-05-10

FILS APPLICATION WURSER: US/02/02-10

SOUTHWAS PARKED OF MINGOUS CO. MINGOW Version 4.0

SOUTHWAS PARKED OF MINGOUS CO. MINGOW VERSION WORLD CO. MINGOUS CO. MINGOUS CO. MINGOUS CO. MINGOW VERSION CO. MINGOUS CO. MIN
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US-09-638-202A-112
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                                                                                               1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                                                     1 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 60
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                                                            0; Gaps
                                                                                                                                                                                                                                                                                                      Sequence 110, Application US/09637614
Patent No. 6703199
GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
                  Score 361; DB 2; Length 94;
Pred. No. 1.8e-35;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 361; DB 2; ilarity 77.7%; Pred. No. 1.8e-35; Conservative 4; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/096,749
PILING DATE: «UNKINOMI»
ATTORNEY/AGENT INPORMATION:
NAME: Ann S. Vikenins
REGISTRATION NUMBER: 37,748
REPERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 339-3061
                                                                                                                                                                                                 61 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                                                                                                                                                                          61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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FILING DATE: 11-Aug-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                    73.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
Query Match
Best Local Similarity 77...
Best Local Similarity 77...
Annual Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MN
COUNTRY: USA
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Best Local Similarity
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                                                                                                                                                                                                                                                                          RESULT 5
US-09-637-614-110
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3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
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                                                                                                                                                                                      ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 96;
US-09-638-202A-112
Sequence 112, Application US/09638202A
Patent No. 6462189
GENERAL IMPORMYION:
GENERAL IMPORMYION:
APPLICANT: Koleda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112, Application US/09096749A

Patent No. 6673901

GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Righth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.1%; Score 361; DB 2; L 77.7%; Pred. No. 1.9e-35; iive 4; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
CCMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,202A
FILING DATE: 11-Aug-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/096,749
FILING DATE: cUNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikenins
REGISTRATION NUMBER: 37,748
REGISTRATION NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                               ZIP: 55402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MN
COUNTRY: USA
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Query Match 73.1%; Score 361; DB 2; Best Local Similarity 77.7%; Pred. No. 1.9e-35; Matches 73; Conservative 4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 112: US-09-637-614-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,683A
FILING DATE: 17-UTM-1993
CLASSIFICATION: 435
ATTORNEY AGENT THORDAMINION:
NAME: VINCENT, MATCHEW P:
REGISTRATION NUMBER: 36,709
REFERENCED POCKET NUMBER: 36,709
REFERENCED POCKET NUMBER: 36,709
REFERENCED FORTEN TOWN:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
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                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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US-08-078-683A-34
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Patent No. 6703199
GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 361; DB 2; Length 96;
Pred. No. 1.9e-35;
4; Mismatches 17; Indels
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                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749A
FILING DATE: Jume 12, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 37,148
FILING DATE: VIKENINS
NAME: AND S. VIKENINS
REGISTRATION NUMBER: 37,748
REPERENCE/DOCKET NUMBER: 37,748
REGISTRATION NUMBER: 37,748
REPERENCE/COCKET NUMBER: 109.034USI
TELEPHONE: (612) 339-3061
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TYPE: maino acid
TYPE: maino acids
TOPOLOGY: linear
TOPOLOGY: linear
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APPLICATION NUMBER: US/09/637,614
FILING DATE: 11.Aug-2000
PRIOR APPLICATION NUMBER: 09/096,749
FILING DATE: -UNKNOWN-
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
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ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: 1
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US-09-637-614-112
COUNTRY:
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3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton
APPLICANT: Bernfield, Merton
TITLE OF INVENTION: Construction and USe of Synthetic
TITLE OF INVENTION: Constructs Encoding Syndecan
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STRATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches 17; Indels
NAME: Ann S. Viksnins

REGISTRATION NUMBER: 37,748

REPERENCE/DOCKET NUMBER: 109.034US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 373-6900

TELEPHONE: (612) 373-691

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 96 anno acids
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APPLICANT: SAUDURES, SUCIT
APPLICANT: SAUDURES, SUCIT
APPLICANT: BERNFIELD, MERTON
APPLICANT: KATO, MASATO
TITLE OF INVERTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
FILE REPERENCE: 10133-151
CURRENT APPLICATION NUMBER: US/09/723,677B
CURRENT PILLING DATE: 1995-06-06
PRIOR FILLING DATE: 1995-06-06
PRIOR PELLOR DATE: 1993-06-17
PRIOR FILLING DATE: 1993-06-17
PRIOR PELLOR DATE: 1993-06-17
PRIOR PELLOR OBJEE: 1991-09-06
PRIOR PELLOR DATE: 1991-09-12
PRIOR PELLOR DATE: 1991-09-06
PRIOR PELLOR DATE: 1991-09-06
PRIOR PELLOR DATE: 1991-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGNSPVOEFTVPPWASIATIS 60
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Patent No. 5302701
GENERAL INFORMATION:
APPLICANT: Hidetaka HASHI et al.
TITLE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 361; DB 2; Length 17
Pred. No. 4.2e-35;
4; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,369 FILING DATE: 19921013 CLASSIFICATION: 530 PRICATION: 530 PRICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C.
                                                                                               Sequence 34, Application US/09723677B Patent No. 6699968 GENERAL INFORMATION:
APPLICANT: SAUNDERS, SCOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: MUS SP;HOMO SAPIEN
US-09-723-677B-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C. COUNTRY: U.S.A.
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                                                                                                                                                                        1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
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                                                                                                                            Gaps
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                                                                     Score 361; DB 1; Length 175;
Pred. No. 4.2e-35;
4; Mismatches 17; Indels
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Pred. No. 4.2e-35;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08471970A
Fatent No. 6531295
GENERAL INFORMATION:
APPLICANT: Saunders, Scott
APPLICANT: Sanders, Scott
TITLE OF INVENTION: Construction and USe of Synthetic
TITLE OF INVENTION: Constructs Encoding Syndecan
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEB: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                      142 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 175
                                                                                                                                                                                                                                                                            61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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CLASSIFICATION: 435
PROGRAPPICATION 04745
PRICATION NUMBER: US 08/078,683
FILING DATE: 17-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P-41,106
REFERENCE/POCKET NUMBER: CME-062DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (teax)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/471,970A
                                                                   Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
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Best Local Similarity 77.7%;
Matches 73; Conservative
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
; PRAGMENT TYPE: internal
US-08-078-683A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-08-471-970A-34
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Gaps

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APPLICANT: Hidetaka HASHI et al.
TITE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: Inal Compatible
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: Diskette, 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,369
FILING DATE: 19921013
CLASSIPTCATION: 530
PRIOR APPLICATION NATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: WAITEN M. Check, JT.
REGISTRATION NUMBER:
TELECOMMUNICATION UNPERF:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: polypeptide
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PEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
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IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CLONE:
CHROMOSOME/SEGMENT:
MAP POSITION:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOLUME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.1%; Score 361; DB 1; Length 256; Best Local Similarity 77.7%; Pred. No. 6.9e-35; Matches 73; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 250
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US-07-959-369-10
is equence 10, Application US/07959369;
Patent No. 5302701
igeneral Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-1
FILING DATE:
ATORNEY/AERT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/POCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITS:
PRATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STACE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL INVE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE:
JOURNAL:
                                                                                                                                                       TELEFAX:
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DOCUMENT NUMBER: FILING DATE: PUBLICATION DATE:

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1 VSDVPRDLEVVAATPTSRLISWNRSGLOSRYYRITYGETGGNSPVQEFTVPPWASIATIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
AITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDLIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIGNE APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTOMARY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 317721/1994
ATTOMARY/AGENT INFORMATION:
NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.1%; Score 361; DB 1; Best Local Similarity 77.7%; Pred. No. 7.6e-35; Matches 73; Conservative 4; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSER: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
GITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: HASHINO=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEYANT RESIDUES IN SEQ ID NO:
US-07-959-369-12
                                                                                                                                                     FEATURE:
NAME/KRY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
                               POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                        TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-836-854-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                     1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGBTGGNSPVQEFTVPPWASIATIS 60
                                                                                                                                                               ö
                                                                                  Score 361; DB 1; Length 258;
Pred. No. 7e-35;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/07959369;
Patent No. 5302701
GENERAL INFORMATION:
TITLE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                              217 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 250
                                                                                                                                                                                                                                                                                                                                           61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER 10005
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: WAS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,369
FILING DATE: 19921013
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT: NFORMATION:
RELEVANT RESIDUES IN SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REPERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 274 amino acids TYPE: AMINO ACID STRANDEDNESS: single
                                                                                            Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAPLOTYPE:
TISSUB TYPE:
CELL TYPE:
CELL LINE:
CELL LINE:
INMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
               US-07-959-369-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-07-959-369-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
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| TELECOMMUNICATION INFORMATION:
| TELEPHONE: (202) 628-5197 |
| TELEPHONE: (202) 737-3528 |
| INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: |
| LENGTH: 274 amino acida |
| TYPE: ```

Search completed: February 23, 2006, 07:49:09 Job time: 47 secs

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US-10-486-512-9

US-10-509-055-15

US-10-509-055-16

US-09-775-964-4

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US-09-775-964-5

US-09-775-964-5

US-09-775-964-5

US-09-775-964-7

US-09-775-964-7

US-09-775-964-7

US-09-775-964-7

US-09-775-964-7

US-09-775-964-1
                                            ~~~~~~~~~
 ; Search time 165 Seconds
(without alignments)
238.036 Million cell updates/sec
 494
1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKXDDPLSINYRT
 GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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February 23, 2006, 07:59:05

60

Run

US-09-688-566-81

Perfect score:

Sequence:

OM protein - protein search, using sw model

Copyright

1867569

Total number of hits satisfying chosen parameters:

1867569 segs, 417829326 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Sequence 1, Application US/10302456
; Bublication No. US20030100004A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; TITLE OF INVENTION: Solid Phase Immobilization of Proteins
; TITLE OF INVENTION: and Peptides
; TITLE OF INVENTION: and Peptides
; FILE REFERENCE: 50036/051002
; CURRENT APPLICATION NUMBER: US/10/302,456
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/333,470
; PRIOR PILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASERE FOR Windows Version 4.0
; SEQ ID NO 1
: LENGTH: 96 ORGANISM: Artificial Sequence

; OTHER INFORMATION: Synthetic Peptide US-10-302-456-1

61 2 VSDVPRDLEVVAATPISLISWKTHEVAARYYRITYGEIGGNSPVQEFTVPPWASIATIS 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS g ð

9

Gaps

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Indels

74.4%; Score 367.5; DB 4; ilarity 80.0%; Pred. No. 5.8e-34; Conservative 3; Mismatches 15;

Query Match Best Local Similarity Matches 76; Conserv

Length 96;

GLKPGVDYTITVYAVTPLRWTETEAHIPIPINYRT 96 61 GLKPGVDYTITVYAVTDKSDT-YKYDDPISINYRT 94

ð g RESULT 2 US-09-096-749A-110

Sequence 110, Application US/09096749A
Fatent No. US20020019517A1
GENERAL INFORMATION:
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq Sequence Sequence S Sequence US-10-486-512-5 US-10-509-055-11 US-09-775-964-24 

16, Appli 4, Appli 22, Appli 11, Appl 17, Appl 17, Appl 21, Appli 12, Appli 12, Appli

## ALIGNMENTS

Published Applications AA Main:\*

1: /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/USIO8\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/USIO8\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/USIO8\_PUBCOMB.pep:\* Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Description                | Sequence 1, Appli | 110                | 110,               | 110,              | 110               |                 | 112                | 110,              | 112,              | 121,              | 112,               | 112,              | 112,              | 2, Ag           | 34,              | 7               | 4,              | 9               | Sequence 25, Appl | ď               | æ               | 5                | 7,              | 13,              | 10,              | 8               | 14,              |
|-----------|----------------------------|-------------------|--------------------|--------------------|-------------------|-------------------|-----------------|--------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-----------------|------------------|-----------------|-----------------|-----------------|-------------------|-----------------|-----------------|------------------|-----------------|------------------|------------------|-----------------|------------------|
|           | ព                          | US-10-302-456-1   | US-09-096-749A-110 | US-10-174-717A-110 | US-10-165-155-110 | US-10-190-162-110 | US-10-509-055-3 | US-09-096-749A-112 | US-09-903-412-110 | US-09-903-412-112 | US-09-903-412-121 | US-10-174-717A-112 | US-10-165-155-112 | US-10-190-162-112 | US-10-006-760-2 | US-10-776-989-34 | US-10-895-590-2 | US-10-895-590-4 | US-10-895-590-6 | US-09-775-964-25  | US-10-486-512-1 | US-10-509-055-8 | US-09-775-964-29 | US-10-486-512-7 | US-10-509-055-13 | US-10-279-733-10 | US-10-486-512-8 | US-10-509-055-14 |
|           | DB                         | 4                 | m                  | 4                  | 4                 | 4                 | ß               | ٣                  | ٣                 | ო                 | m                 | 4                  | 4                 | 4                 | 4               | Ŋ                | Ŋ               | Ŋ               | Ŋ               | ო                 | 2               | 'n              | m                | ស               | 2                | 4                | Ŋ               | Ŋ                |
| •         | *<br>Query<br>Match Length | 96                | 94                 | 94                 | 94                | 94                | 94              | 96                 | 96                | 96                | 96                | 96                 | 96                | 96                | 96              | 175              | 184             | 184             | 184             | 274               | 274             | 274             | 302              | 302             | 302              | 330              | 367             | 367              |
| ,         | Query<br>Match             | 74.4              | 73.1               | 73.1               | 73.1              | 73.1              | 73.1            | 73.1               | 73.1              | 73.1              | 73.1              | 73.1               | 73.1              | 73.1              | 73.1            | 73.1             | 73.1            | 73.1            | 73.1            | 73.1              | 73.1            | 73.1            | 73.1             | 73.1            | 73.1             | 73.1             | 73.1            | 73.1             |
|           | Score                      | 367.5             | 361                | 361                | 361               | 361               | 361             | 361                | 361               | 361               | 361               | 361                | 361               | 361               | 361             | 361              | 361             | 361             | 361             | 361               | 361             | 361             | 361              | 361             | 361              | 361              | 361             | 361              |
|           | Result<br>No.              | -                 | 7                  | m                  | 4                 | S                 | 9               | 7                  | 80                | 0                 | 10                | 11                 | 12                | 13                | 14              | 15               | 16              | 17              | 18              | 19                | 20              | 21              | 22               | 23              | 24               | 25               |                 | 27               |

```
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 110:
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
 LENGTH: 94 amino acids
 ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 TYPE: amino acid
STRANDEDNESS: single
 SEQUENCE CHARACTERISTICS
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 COUNTRY: USA
 US-10-174-717A-110
 RESULT 4
US-10-165-155-110
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 1 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 60
 Sequence 110, Application US/10174717A
Publication No. US20030108948A1
APPLICANT: Koide, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, St. 1600
 Query Match 73.1%; Score 361; DB 3; Length 94; Best Local Similarity 77.7%; Pred. No. 3.1e-33; Matches 73; Conservative 4; Mismatches 17; Indels
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 61 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 94
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,717A
FILING DATE: 18-Jun-2002
PRIOR APPLICATION DATA:
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikenins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELEPOOMUNICATION INFORMATION:
TELEPONE: (612) 373-6900
TELEPAX: (612) 335-3061
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
 OPERATING SYSTEM: OBSERVING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749A FILING DATE: June 12, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 APPLICATION NUMBER: 09/096,749
FILING DATE: June 12, 1998
APPLICATION NUMBER: 60/049,410
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
 COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FastSEQ Version 2.0b
 MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
 ZIP: 55402
COMPUTER READABLE FORM:
 internal
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 MOLECULE TYPE: peptide HYPOTHETICAL: NO
 STATE: MN
COUNTRY: USA
 FRAGMENT TYPE:
 ANTI-SENSE: NO
 HYPOTHETICAL:
 US-09-096-749A-110
 US-10-174-717A-110
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1 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 60
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Gaps
 ;
0
 Sequence 110, Application US/10165155
Publication No. US20030134386A1
GENERAL INFORMATION:
APPLICANT: Koleda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 112 South Righth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
 Length 94;
 17; Indels
 Query Match 73.1%; Score 361; DB 4; Best Local Similarity 77.7%; Pred. No. 3.1e-33; Matches 73; Conservative 4; Mismatches 17
 CURRENTING SYSTEM COMPACTURE
COMPUTER: IBM COMPACTURE
COPEMATING SYSTEM: DOS
SOFTWARE: FESTESEQ VERSION 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,155
FILING DATE: 06-Jun-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749
FILING DATE: June 12, 1998
ATTORNEY/AGENT INPORMATION:
NAME: ALD S. VIKENINS
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034USI
TELECOMMUNICATION:
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
REGISTRATION NUMBER: 37,748
REPERBNUE/COCKET NUMBER: 109.034US4
TELECOMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEPAX: (612) 33-3061
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 aming acids
 ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
```

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1 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 60
 REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
FELECOMMUNICATION INFORMATION:
 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISTO Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,746
FILING DATE: June 12, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 TYPE: PRT
ORGANISM: Artificial Sequence
 FILING DATE: ATTORNEY/AGENT INFORMATION:
 Query Match
Best Local Similarity 77.7<sup>1</sup>
Matches 73; Conservative
 NAME: Ann S. Vikenins
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 USA
 US-09-096-749A-112
 55402
 US-10-509-055-3
 COUNTRY:
 US-10-509-055-3
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 1 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 60
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Gaps
 .
0
 Sequence 110, Application US/10190162
Publication No. US20030170753A1
GENERAL INPORMATION:
APPLICANT: Koica, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
 Score 361; DB 4; Length 94;
Pred. No. 3.1e-33;
4; Mismatches 17; Indels
 ch 73.1%; Score 361; DB 4; Length 94; Similarity 77.7%; Pred. No. 3.1e-33; 73; Conservative 4; Mismatches 17; Indels
 CURRENT APPLICATION DATE:

APPLICATION NUMBER: US,10/190,162
FILING DATE: 03-011-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US,09/096,749
FILING DATE: June 12, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikenins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 94
 ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-165-155-110
 ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
 ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPR: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0b
 TELEPHONE: (612) 373-6900
 (612) 339-3061
 LENGTH: 94 amino acids
 INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
STRANDEDNESS: single
 Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
 FRAGMENT TYPE: internal
 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
 COUNTRY: USA
HYPOTHETICAL: NO
 Best Local Similarity
 STATE: MN
 JS-10-190-162-110
 Query Match
 Matches
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLOSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Gaps
 ; Sequence 3, Application US/10509055; Publication No. US20050227354A1; GENERAL INFORMATION:
APPLICANT: SAGAWA, Hiroaki et al., APPLICANT: SAGAWA, Hiroaki et al., TILLE OF INVENTION: PROCESS FOR PRODUCING CYTOTOXIC LYMPHOCYTE; TILLE OF INVENTION: PROCESS FOR PRODUCING CYTOTOXIC LYMPHOCYTE; CURRENT APPLICATION NUMBER: US/10/509,055; CURRENT FILING DATE: 2004-09-24; PRIOR APPLICATION NUMBER: PCT/JP03/03575; NUMBER OF SEQ ID NOS: 24; SOFTWARE: Patent-In 3.3; SEQ ID NO 3; LENGTH: 94
 ö
 OTHER INFORMATION: partial region of fibronectin named III-10
 73.1%; Score 361; DB 5; Length 94; 77.7%; Pred. No. 3.1e-33; tive 4; Mismatches 17; Indels
 Sequence 112, Application US/09096749A

Patent No. US20020019517A1

GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
ITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: Mineapolis
STATE: MN.
61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 61 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT
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 9
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
 3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
 1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Gaps
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 Score 361; DB 3; Length 96;
Pred. No. 3.2e-33;
4; Mismatches 17; Indels
 Score 361; DB 3; Length 96; Pred. No. 3.2e-33; 4; Mismatches 17; Indels
 US-09-903-412-110
; Sequence 110, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION: AS APPLICANT KOIDE, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; FILE REFERENCE: 109.0501031
; CURRENT APPLICATION NUMBER: US/09/903,412
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ 1D NOS: 121
; SOFTWARE: FREESEQ for Windows Version 4.0
 APPLICANT: Koide, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
FILE REPERENCE: 109.050USI
CURRENT APPLICATION UNMER: US/09/903,412
CURRENT FILING DATE: 2001-07-11
 63 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
 63 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 ; FEATURE:
; OTHER INFORMATION: The synthetic Fn3 gene.
US-09-903-412-110
 RESULT 9
US-09-903-412-112
Sequence 112, Application US/09903412
Publication No. US20030027319A1
GENERAL INFORMATION:
 Query Match
Best Local Similarity 77.7%;
Matches 73; Conservative
(612) 373-6900
 Query Match
Best Local Similarity 77.7%;
Matches 73; Conservative
 TYPE: PRT
ORGANISM: Artificial Sequence
 TELEPAX: (612) 339-3061
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
 internal
 TYPE: amino acid
STRANDEDNESS: single
 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
 FRAGMENT TYPE: i
; ORIGINAL SOURCE:
US-09-096-749A-112
 ANTI-SENSE: NO
TELEPHONE:
 SEQ ID NO 110
LENGTH: 96
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 62
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 62
 3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS
 3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS
 1 VSDVPRDLEVVAATPTSRLISWNRSGLOSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 ö
 Sequence 112, Application US/10174717A
Publication No. US20030108948A1
APPLICANT: Koide, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, St. 1600
CITY: Minneapolis
 Length 96;
 73.1%; Score 361; DB 3; Length 96; 77.7%; Pred. No. 3.2e-33;
 4; Mismatches 17; Indels
 Sequence 121, Application US/09903412
Publication No. US20030027319A1
GENERAL INFORMATION:
APPLICANT: Koids Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
FILE REFERENCE: 109.050US1
CURRENT APPLICATION NUMBER: US/09/903,412
CURRENT FILING DATE: 2001-07-11
PRIOR FILING DATE: 2000-07-11
 Query Match 73.1%; Score 361; DB 3; Best Local Similarity 77.7%; Pred. No. 3.2e-33; Matches 73; Conservative 4; Mismatches 17
 63 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
PRIOR APPLICATION NUMBER: US 60/217,474
PRIOR FILING DATE: 2000-07-11
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 112
LENGTH: 96
 ; OTHER INFORMATION: The designed Fn3 gene. US-09-903-412-112
 NUMBER OF SEQ ID NOS: 121
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 121
LENGTH: 96
 ORGANISM: Artificial Sequence
 ZIP: 55402
COMPUTER READABLE FORM:
 Query Match
Best Local Similarity 77...
Best Local Similarity 77...
The T3; Conservative
 STATE: MN
COUNTRY: USA
 TYPE: PRT
ORGANISM: Homo sapiens
 RESULT 11
US-10-174-717A-112
 RESULT 10
US-09-903-412-121
 US-09-903-412-121
 FEATURE:
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3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Sequence 112, Application US/10190162
Publication No. US20030170753A1
GENERAL INFORMATION:
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
STATE: ADDRESSE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
 Query Match 73.1%; Score 361; DB 4; Length 96; Best Local Similarity 77.7%; Pred. No. 3.2e-33; Matches 73; Conservative 4; Mismatches 17; Indels
 COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/190,162
FILING DATE: 03-Jul-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749
FILING DATE: June 12, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. VİKBRINB
REGISTRATION NUMBER: 37,748
REFERRENCE/DOCKET NUMBER: 109.034USI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 63 GLKPGVDÝTÍTVÝAVTGRGDSPASSKPISÍNÝRŤ 96
NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
 TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-165-112
 TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 aming acids
 TELEFAX: (612) 339-3061
 INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
 ZIP: 55402
COMPUTER READABLE FORM:
 MOLECULE TYPE: peptide
 USA
 COUNTRY:
 US-10-190-162-112
 RESULT 13
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 Gaps
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 Sequence 112, Application US/10165155
Publication No. US20030134386A1
GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
 Score 361; DB 4; Length 96;
Pred. No. 3.2e-33;
4; Mismatches 17; Indels
 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,717A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/096,749
FILING DATE: June 12, 1998
APPLICATION NUMBER: 60/049,410
FILING DATE: June 12, 1997
ATTORNEY/AGNT INFORMATION:
NAME: Ann S. VİKSHİJIS
REGISTRATION NUMBER: 37,748
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
 APPLICATION NUMBER: US/09/096,749 FILING DATE: June 12, 1998 ATTORNEY/AGENT INFORMATION:
 COMPUTER: IEM Compatible
OPERATIOS SYSTEM: DOS
SOFTWARE: FREISEO VETRION 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,155
PRIOR APPLICATION DATA:
 ANTI-SENSE: NO
PRAGMENT TYPES: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
 TELEFAX: (612) 339-3061
 INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
 COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 73.1%;
 Query Match
Best Local Similarity 77.7-
Best Local Similarity 77.7-
Taylor Taylor Conservative
 STATE: MIN
 JS-10-174-717A-112
 US-10-165-155-112
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 HESULT 15
US-10-776-989-34

Sequence 34, Application US/10776989

Publication No. US20050075484A1

GENERAL INFORMATION:
APPLICANT: SAUUDERS, SCOTT

APPLICANT: BERNFIELD, MERTON
FILE REFERENCE: 101353-232

CURRENT APPLICATION NUMBER: US/10/776,989

CURRENT APPLICATION NUMBER: 09/723,677

PRIOR PILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: 08/471,970

PRIOR APPLICATION NUMBER: 08/471,970

PRIOR PILING DATE: 1993-06-06

PRIOR FILING DATE: 1993-06-17

PRIOR PILING DATE: 1993-06-17

PRIOR FILING DATE: 1993-06-17
 ö
 TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF CURRENT APPLICATION NUMBER: US/10/006,760 CURRENT FILING DATE: 2001-11-19 PRIOR APPLICATION NUMBER: 60/249,756 PRIOR PRILING DATE: 2000-11-17 NUMBER OF SEQ ID NOS: 73 SOFTWARE: PACENTIN VET: 2.1 SEQ ID NO: 2.2 SEQ ID NO: 2.1 SEQ ID NO
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
 1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
 Gaps
 Gaps
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 Query Match 73.1%; Score 361; DB 4; Length 96; Best Local Similarity 77.7%; Pred. No. 3.2e-33; Matches 73; Conservative 4; Mismatches 17; Indels
 Query Match 73.1%; Score 361; DB 4; Length 96; Best Local Similarity 77.7%; Pred. No. 3.2e-33; Matches 73; Conservative 4; Mismatches 17; Indels
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 63 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
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 ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-190-162-112
 Sequence 2, Application US/10006760 Publication No. US20030186385A1 GENERAL INFORMATION:
 , ORGANISM: Homo sapiens
US-10-006-760-2
HYPOTHETICAL: NO
 RESULT 14
US-10-006-760-2
 TYPE: PRT
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82 VSDVPRDLEVVAATPTSLLISWDAPAVTVRXYRITYGETGGNSPVQEFTVPGSKSTATIS 141
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 Gaps
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 Length 175;
 17; Indels
 Score 361; DB 5;
Pred. No. 6.7e-33;
4; Mismatches 17,
 142 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 175
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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PRIOR FILING DATE: 1992-03-24

PRIOR PLING DATE: 1991-09-06

PRIOR PLING DATE: 1991-09-06

PRIOR APPLICATION NUMBER: 07/746,797

PRIOR PILING DATE: 1991-08-12

PRIOR PAPLICATION NUMBER: 07/331,585

PRIOR PLING DATE: 1999-03-29

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin version 3.0

SEQ ID NO 34

LENGTH: 175

TYPE: PRI

TYPE: PRI

CREANISM: MUS SP,HOMO SAPIEN

US-10-776-989-34
 Query Match
Best Local Similarity 77.7%;
Matches 73; Conservative
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1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKYDDPISINYRT
 Published Applications AA New:*

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2: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USI0_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USI0_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USI1 NEW_PUB.pep:*
GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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 Total number of hits satisfying chosen parameters:
 117670 seqs, 14887254 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 February 23, 2006, 08:01:29
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-688-566-81
 Copyright
 Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

|           | Description           | Sequence 25, Appl | 29               | 4               | 'n              | 22               | Sequence 7, Appli | 21               | æ               | 23               | 24               | 14               | 63                | Sequence 625, App | 62                | Sequence 630, App | 62                | Sequence 624, App | 25               | Sequence 25, Appl | 25               | Sequence 25, Appl | Sequence 25, Appl | Seguence 38, Appl | 38,       | Sequence 38, Appl |
|-----------|-----------------------|-------------------|------------------|-----------------|-----------------|------------------|-------------------|------------------|-----------------|------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|------------------|-------------------|-------------------|-------------------|-----------|-------------------|
| SUMMARIES | ID                    | US-11-181-091-25  | US-11-181-091-29 | US-11-181-091-4 | US-11-181-091-5 | US-11-181-091-22 | US-11-181-091-7   | US-11-181-091-21 | US-11-181-091-8 | US-11-181-091-23 | US-11-181-091-24 | US-11-181-091-14 | US-10-995-561-634 | US-10-995-561-625 | US-10-995-561-628 | US-10-995-561-630 | US-10-995-561-621 | US-10-995-561-624 | US-11-193-561-25 | US-11-193-771-25  | US-11-193-789-25 | US-11-193-806-25  | US-11-193-857-25  | US-11-193-561-38  | -11 - 193 | US-11-193-789-38  |
|           | DB                    | 7                 | 7                | 7               | 7               | 7                | 7                 | 7                | ^               | 7                | 7                | 7                | 9                 | 9                 | ø                 | 9                 | 9                 | 9                 | 7                | 7                 | 7                | 7                 | 7                 | 7                 | 7         | 7                 |
|           | Query<br>Match Length | 274               | 302              | 432             | 457             | 457              | 464               | 472              | 489             | 549              | 574              | 826              | 847               | 1259              | 1286              | 1315              | 1341              | 1348              | 2176             | 2176              | 2176             | 2176              | 2176              | 2217              | 2217      | 2217              |
| de        | Query<br>Match        | 73.1              | 73.1             | 73.1            | 73.1            | 73.1             | 73.1              | 73.1             | 73.1            | 73.1             | 73.1             | 73.1             | 73.1              | 73.1              | 73.1              | 73.1              | 73.1              | 73.1              | 73.1             | 73.1              | 73.1             | 73.1              | 73.1              | 73.1              | 73.1      | 73.1              |
|           | Score                 | 361               | 361              | 361             | 361             | 361              | 361               | 361              | 361             | 361              | 361              | 361              | 361               | 361               | 361               | 361               | 361               | 361               | 361              | 361               | 361              | 361               | 361               | 361               | 361       | 361               |
|           | Result<br>No.         | 1                 | 7                | m               | 4               | 2                | 9                 | 7                | 80              | 6                | 10               | 11               | 12                | 13                | 14                | 15                | 16                | 17                | 18               | 19                | 20               | 21                | 22                | 23                | 24        | 25                |

Hashino, Kimikazu Kato, Ikunoshin TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091

FILING DATE: 14-Jul-2005

CLASSIFCATION: cunchown.

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/75,964

FILING DATE: 20-Feb-2001

APPLICATION NUMBER: 08/09/366,009

FILING DATE: 02-Aug-1999

APPLICATION NUMBER: 08/09/156

FILING DATE: 13-NOV-1995

APPLICATION NUMBER: JP 294382/1995

APPLICATION NUMBER: JP 294382/1996 NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763 REFERENCE/DOCKET NUMBER: 977.6507P TELECOMMUNICATION INFORMATION: Sequence 25, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION:
HAPPLICANT: Asada, Kiyozo
GENORAL OFFICANT: Asada, Kiyozo
HOROCI, TAKASHI
HOROCI, TAKASHI
KOYAMA, NOBUTO TELEPHONE: 215-875-8383 TELEFAX: 215-875-8394 ATTORNEY/AGENT INFORMATION COUNTRY: USA US-11-181-091-25

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US-11-181-091-4
 RESULT 3
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 g
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 ö
 Kato, Ikunoshin
INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 73.1%; Score 361; DB 7; Length 274; 77.7%; Pred. No. 4.4e-32;
 4; Mismatches 17; Indels
 ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
 238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 CELLS WITH RETROVIRUS
 APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
APPLICATION NUMBER: 08/809,156
FILING DATE: cUnknown>
APPLICATION NUMBER: UP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: UP 294382/1995
APPLICATION NUMBER: UP 051847/1996
 NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOCY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-Jul-2005
CLASSIFICATION: <u >Unknown>
 Sequence 29, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION;
GENERAL INFORMATION;
HOPPLICANT: Asada, Kiyozo
Uemori, Takashi
Uemori, Takashi
HOPPLICANT: HASHI
HOPPLICANT: HASHI
HOPPLICANT: HASHI
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
 FILING DATE: 08-MAR-1996 ATTORNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS
 PRIOR APPLICATION DATA:
 Local Similarity 77.7 tes 73; Conservative
 RESULT 2
US-11-181-091-29
 US-11-181-091-25
 Query Match
 Matches
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 178 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 237
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 ;
0
 Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
 COMPUTER READABLE FORM:

MEDIUM TYPER: RIOPOY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091

PILING DATE: 14-Jul-2005

CLASSIFICATION NUMBER: US/09/75,964

PILING DATE: 20-Feb-2001

APPLICATION NUMBER: US/09/366,009

FILING DATE: 02-ABG-1999

APPLICATION NUMBER: US/09/366,009

PILING DATE: CURLOWN:
APPLICATION NUMBER: US/09/366,009

FILING DATE: CURROWN:
APPLICATION NUMBER: US/09/366,009

FILING DATE: 02-ABR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Weiser: 08-MBR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Weiser: Gerard J.

RESTERENCE/DOCKET NUMBER: 19763

RETERENCE/DOCKET NUMBER: 19763

TELECOMMUNICATION NUMBER: 19763

RETERENCE/DOCKET NUMBER: 19763

TELECOMMUNICATION NUMBER: 19763

RETERENCE/DOCKET NUMBER: 19763

TELECOMMUNICATION NUMBER: 19763

RETERENCE/DOCKET NUMBER: 19763

TELEDROWNEY/AGENT NUMBER: 19763

TELEDROWNEY/AGENT NUMBER: 19763

TELEBRHONE: 215-875-8383
 Length 302;
 Indels
 NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
 73.1%; Score 361; DB 7; 77.7%; Pred. No. 4.9e-32; iive 4; Mismatches 17
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-11-181-091-29
 Sequence 4, Application US/11181091
; Sequence 4, Application US/20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; USMOCI, Takashi
; UGMOCI, Takashi
; Koyama, Nobuto
LENGTH: 302 amino acids
 LENGTH: 432 amino acids
TYPE: amino acid
 TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 Query Match 73.1.
Best Local Similarity 77.7
Matches 73, Conservative
 COUNTRY: USA
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RESULT
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 1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRIIYGETGGNSPVQEFTVPPWASIATIS 60
 Gaps
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 Koyama, Nobuto
Royama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
 Score 361; DB 7; Length 432;
Pred. No. 7.5e-32;
4; Mismatches 17; Indels
 COMPUTER KEALABLE FOURT

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091

FILING DATE: 14-Jul-2005

CLASSIFICATION NUMBER: US/09/75,964

FILING DATE: 20-Peb-2001

APPLICATION NUMBER: US/09/366,009

FILING DATE: 20-Peb-2001

APPLICATION NUMBER: 08/09/366,009

FILING DATE: 13-NOV-1995

APPLICATION NUMBER: 0F 294382/1995

FILING DATE: 13-NOV-1995

APPLICATION NUMBER: UP 294382/1996

FILING DATE: 13-NOV-1996

FILING DATE: 13-NOV-1996

ATTORNEY AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
 238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-181-091-4
 TELECOMMUNICATION INFORMATION
 5-11-181-091-5
Sequence 5, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
STRANDEDNESS: <Unknown>
 Uemori, Takashi
Ueno, Takashi
 INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
 NUMBER OF SEQUENCES: 39
 COMPUTER READABLE FORM:
 FOPOLOGY: linear
 COUNTRY: USA
 ZIP: 19102
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9
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Gaps
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 Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 DB 7; Length 457;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
 73.1%; Score 361; DB 7; L 77.7%; Pred. No. 8e-32; cive 4; Mismatches 17;
 238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: -CURROWN-
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
 ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-011-2005
CLASSIFICATION: <UNKNOWN>
 REFERENCE/DOCKET NUMBER: 977.6507P
 TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
i MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-181-091-5
 NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-675-8393
TELEPAX: 215-675-8394
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
 ATTORNEY/AGENT INFORMATION:
 Uemori, Takashi
Ueno, Takashi
Koyama, Nobuto
 CITY: Philadelphia
 NUMBER OF SEQUENCES: 39
 US-11-181-091-22
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 1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Gaps
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 Sequence 7, Application US/11181091
Sequence 7, Application US/11181091
Sequence 7, Application US/20060030046A1
GENERAL INFORMATION:
GENERAL INFORMATION:
Takashi
Usmo, Takashi
Usmo, Takashi
Kato, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: CELLS WITH RETROVIRUS
 DB 7; Length 457;
 Score 361; DB 7; Length 45:
Pred. No. 8e-32;
4; Mismatches 17; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
 238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 PRIOR APPLICATION NUMBER: US/09/775,964
FILING DATE: 20.Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: 40ARNOWN
APPLICATION NUMBER: UP 294382/1995
FILING DATE: 40ARNOWN-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT: INFORMATION:
 NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
 APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-Jul-2005
CLASSIFICATION: <Unknown>
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 ;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-11-181-091-7
 TELECOMMUNICATION INFORMATION
 SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 7:
 Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES:
 COUNTRY: USA
JS-11-181-091-22
 RESULT 6
US-11-181-091-7
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Gaps
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 Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
 Length 464;
 Length 472;
 Indels
 Version #1.30
 ADDRESSEE: WEISER & ASSOCIATES
STRET: 230 South Fifteenth Street, Suite 500
STATE: Philadelphia
STATE: PA
Score 361; DB 7; Le
Pred. No. 8.1e-32;
1; Mismatches 17;
 Score 361; DB 7;
Pred. No. 8.3e-32;
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091
PILING DATE: 14-011-2005
CLASSIFICATION ATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 20-F6b-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: CURROWN:
APPLICATION NUMBER: US/09/156
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR.1996
 4; Mismatches
 NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
 ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-11-181-091-21
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
 NS-11-181-091-21

Sequence 21, Application US/11181091

Publication No. US20060310046A1

GENERAL INFORMATION:

APPLICANT: Asada, Kiyozo
 TYPE: amino acid
STRANDEDNESS: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 Uemori, Takashi
Ueno, Takashi
Koyama, Nobuto
 Takashi
 73.18;
77.78;
Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
 INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 COUNTRY: USA
 Query Match
Best Local Similarity
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178 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 237
 ö
 Koyama, Nobuto
Royama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
 Length 549;
 17; Indels
 CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
 Query Match 73.1%; Score 361; DB 7; Best Local Similarity 77.7%; Pred. No. 9.8e-32; Matches 73; Conservative 4; Mismatches 17;
 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: CURKNOWN>
APPLICATION NUMBER: JP 294382/1995
APPLICATION NUMBER: JP 294382/1995
APPLICATION NUMBER: JP 294382/1995
APPLICATION NUMBER: JP 995847/1996
FILING DATE: 08-MAR-1996
 NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-11-181-091-23
 Sequence 23, Application US/11181091; Publication No. US20060030046A1; GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
UGMOOTI, Takashi
 LENGTH: 549 amino acids TYPE: amino acid
 215-875-8383
 ATTORNEY/AGENT INFORMATION
 TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS
 CITY: Philadelphia STATE: PA
 SEQUENCES:
 COUNTRY: USA
 TELEPHONE:
 NUMBER OF
 JS-11-181-091-23
 238
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
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 Koyama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
 73.1%; Score 361; DB 7; Length 489; 77.7%; Pred. No. 8.6e-32; Live 4; Mismatches 17; Indels
17; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Pifteenth Street, Suite 500
 238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-701-2005
CLASSIFICATION: UBARDOWN>
PRIOR APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: 3-NOV-1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 294382/1995
APPLICATION NUMBER: JP 294382/1995
APPLICATION NUMBER: JP 051847/1996
PILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
4; Mismatches
 NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
 MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-11-181-091-8
 Sequence 8, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
 LENGTH: 489 amino acida
TYPE: amino acid
 STRANDEDNESS: <Unknown>
 FELEFAX: 215-875-8394
 Uemori, Takas
Ueno, Takashi
 SEQUENCE CHARACTERISTICS
 SEQUENCES: 39
 CITY: Philadelphia
 ZIP: 19102
UTER READABLE FORM:
 INFORMATION FOR SEQ ID NO: 8
 COPOLOGY: linear
 Query Match
Best Local Similarity 77.7
Matches 73; Conservative
73; Conservative
 COUNTRY: USA
 NUMBER OF
 US-11-181-091-8
 61
Matches
 RESULT
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 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
 Gaps
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 Koyama, Nobuto
Hashino, Kimikazu
Kato, Ikunshino FOR GENE TRANSFER INTO TARGET
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 Length 826;
 Indels
 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
 Score 361; DB 7;
Pred. No. 1.6e-31;
4; Mismatches 17,
 238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-UU1-2005
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
 FILING DATE: 02-Aug-1999
PPILING DATE: 02-Aug-1999
FILING DATE: «Unknown»
APPLICATION NUMBER: JP 294382/1995
 FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
 REFERENCE/DOCKET NUMBER: 977.6507P
 LENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
 Sequence 14, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
UEMOCI, Takashi
 ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 TELECOMMUNICATION INFORMATION
 ATTORNEY/AGENT INFORMATION
 73.1%;
 SEQUENCE CHARACTERISTICS
 INFORMATION FOR SEQ ID NO: 14
 NUMBER OF SECUENCES: 39
 Query Match
Best Local Similarity 77.7
Matches 73; Conservative
 USA
 COUNTRY:
 US-11-181-091-14
 US-11-181-091-14
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 178 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVORFTVPGSKSTATIS 237
178 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 237
 VSDVPRDLEVVAATPTSRLISWNRSGLOSRYYRITYGETGGNSPVQEPTVPPWASIATIS
 Gaps
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 Koyama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
 DB 7; Length 574;
 Score 361; DB 7; Length 57.
Pred. No. 1e-31;
4; Mismatches 17; Indels
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PatentIn Release #1.0, Version #1.30
ENT APPLICATION DATA:
PILING DATE: 14-Jul-2005
CLASSIFICATION: <UNKnown>
 CORRESPONDENCE ADDRESS:
ADDRESSER: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
 238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
 94
 PRIOR APPLICATION NUMBER: US/09/775,964
PILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: Charlown:
APPLICATION NUMBER: UP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: UP 294382/1995
FILING DATE: 08-MAR-1996
 REFERENCE/DOCKET NUMBER: 977.6507P
 MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
 NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763
 Sequence 24, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
 TELECOMMUNICATION INFORMATION TELEPHONE: 215-875-8383
 STRANDEDNESS: <Unknown>
TOPOLOGY: linear
 ATTORNEY/AGENT INFORMATION
 APPLICANT: Asada, Kiyozo
Uemori, Takashi
 TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
 Uemori, Takas
Ueno, Takashi
 Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
 NUMBER OF SEQUENCES: 39
 COMPUTER READABLE FORM:
 TYPE: amino acid
 ZIP: 19102
 CURRENT
 RESULT 10
US-11-181-091-24
 JS-11-181-091-24
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241 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 274

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LENGTH: 1315
 61
 TYPE: PRT
 TYPE: PRT
 LENGTH:
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 Sequence 634, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michel et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 634
 ö
 Sequence 625, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DATECTION AND USES THEREOF
TITLE OF INVENTION: UNMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PARKEOF FOR Windows Version 4.0
 165 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 224
 1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
 Gaps
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 73.1%; Score 361; DB 6; Length 1259; 77.7%; Pred. No. 2.6e-31; ive 4; Mismatches 17; Indels (
 Query Match
Pest Local Similarity 77.7%; Pred. No. 1.6e-31;
Matches 73; Conservative 4; Mismatches 17; Indels
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US-10-995-561-634
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US-10-995-561-634
 US-10-995-561-625
 73;
 US-10-995-561-625
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RESULT 14 US-10-995-561-628 Sequence 628, Application US/10995561 ; Publication No. US20050272054A1

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Sequence 630, Application US/10995561
Publication No. US2005272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: CARDILL, Michel et al.
TITLE OF INVENTION: CARDICVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: B1001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
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SEQ ID NOS: 85702
SEQ ID NOS: 85702
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILLIG DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

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US-10-995-561-628
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